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**"Examiner Search Notes"**

Thank you.

James Martinell  
Primary Examiner 1631

**This Page Blank (uspto)**

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OM nucleic - nucleic search, using sw model

Run on: February 26, 2005, 01:43:47 ; Search time 210.069 Seconds  
(without alignments)  
8342.279 Million cell updates/sec

Title: US-09-938-842a-1034

Perfect score: 1071  
Sequence: 1 atggcgacacatcagacagct.....cagcgatcagacacacga 1071

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/6C\_COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfillseq1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	4.1	7218	1	US-08-232-463-14
2	41	3.8	7218	1	US-08-232-463-14
3	40.4	3.8	915	4	US-09-248-796A-6057
4	34	3.2	654	4	US-08-956-171E-613
5	34	3.2	654	4	US-08-781-986A-613
6	33.4	3.1	601	4	US-09-949-016-33921
7	33.4	3.1	601	4	US-09-949-016-133049
8	33.4	3.1	34068	4	US-09-949-016-15489
9	33.4	3.1	51721	4	US-09-949-016-12559
10	33	3.1	2127	4	US-09-252-991A-8192
11	33	3.1	2874	4	US-09-252-991A-8112
12	32.8	3.1	4403765	3	US-09-103-840A-2
13	32.2	3.0	2406	3	US-09-632-098-5
14	32.2	3.0	2406	4	US-10-177-308-5
15	32.2	3.0	2439	3	US-09-632-098-6
16	32.2	3.0	2439	4	US-10-177-308-6
17	31.6	3.0	601	4	US-09-949-016-121693
18	31.6	3.0	601	4	US-09-949-016-121694
19	31.6	3.0	601	4	US-09-949-016-121695
20	31.6	3.0	1104	4	US-09-902-540-6871
21	31.6	3.0	1141	4	US-09-806-708B-22
22	31.6	3.0	4019	4	US-09-902-540-583
23	31.6	2.9	15192	4	US-09-949-016-15143
24	31.4	2.9	4411529	3	US-09-103-840A-1
25	30.6	2.9	3842	4	US-09-976-594-279
26	30.6	2.9	412	3	US-08-961-083-111
27	30.6	2.9	412	4	US-09-536-784-111

C 28	30.6	2.9	894	4	US-09-540-236-1485	Sequence 1485, Ap
C 29	30.6	2.9	912	4	US-09-489-039A-3905	Sequence 3905, Ap
C 30	30.6	2.9	963	4	US-09-270-767-2582	Sequence 2582, Ap
C 31	30.6	2.9	963	4	US-09-270-767-1864	Sequence 1764, A
C 32	30.6	2.9	1288	4	US-09-620-312D-546	Sequence 546, App
C 33	30.6	2.9	2322	4	US-09-270-767-1512	Sequence 1512, Ap
C 34	30.6	2.9	2322	4	US-09-270-767-16794	Sequence 16794, A
C 35	30.6	2.9	2427	4	US-09-270-767-4937	Sequence 4937, Ap
C 36	30.6	2.9	2427	4	US-09-270-767-20219	Sequence 20219, A
C 37	30.6	2.9	6693	3	US-08-961-527-195	Sequence 195, App
C 38	30.6	2.9	49617	4	US-09-596-002-28	Sequence 28, App
C 39	30.6	2.9	250715	4	US-09-949-016-13294	Sequence 13294, A
C 40	30.4	2.8	2172	1	US-07-982-712-1	Sequence 1, App11
C 41	30.4	2.8	7766	3	US-09-125-619-3	Sequence 3, App11
C 42	30.4	2.8	7766	4	US-10-222-566-3	Sequence 3, App11
C 43	30.4	2.8	7766	4	US-10-143-024A-3	Sequence 3, App11
C 44	30.4	2.8	580073	4	US-08-545-528D-1	Sequence 1, App11
C 45	30.2	2.8	306	4	US-09-513-999C-11186	Sequence 1186, A

#### ALIGNMENTS

RESULT 1  
US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHIEFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232,463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935,313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29, 768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-9300  
; TELEFAX: (703) 683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: PTZpct-F18  
; US-08-232-463-14  
Query Match 4.1%; Score 44; DB 1; Length 7218;

Best Local Similarity 2.3%; Pred. No. 0.0023;  
Matches 8; Conservative 203; Mismatches 143; Indels 0; Gaps 0;

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QY 542 CCGTTACAGCTCTCCGCTTTAGCTCCAAATGCCAGCAGCAGCAGCAGCAGCTCCGCG 601
Db 1093 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1152
QY 602 AAGCTCTGCATCATCATGCTGAGCTGAGCAGCTTCCGCGCAGAGAAATGATCCAGT 661
Db 1153 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1212
QY 662 GGGTATTCATCAACGCAATGATTCGACGCTGAGCTTCTTGTGATTCACAA 721
Db 1213 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1272
QY 722 TCGTGGTCCGCTGAATCAGCTCAGTATAGCTTTCCGCGCGCTGCTGCGCT 781
Db 1273 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1332
QY 782 CGCTTACGTCGCGCTGTTCACAGAGCTTCACAGATGCTGACACACTCCTTACAG 841
Db 1333 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1392
QY 842 TTGTTCCAGCAGCGGCTTGTATCCGTTTCAGAGCTTACGCTTGAATTTAT 895
Db 1393 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1446
```

## RESULT 2

US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHIEFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMM  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEO ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

IMMEDIATE SOURCE:  
CLONE: pTZgpc-F18  
US-08-232-463-14

Query Match 3.8%; Score 41; DB 1; Length 7218;  
Best Local Similarity 2.2%; Pred. No. 0.024;  
Matches 8; Conservative 205; Mismatches 150; Indels 0; Gaps 0;

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QY 195 GACAGACCAACCAATTGAAGAGCTTGCATTAAGACCTCACAGCAGGTGAAGAG 254
Db 1414 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1355
QY 255 AGGAGAGAGATACGATGCTCCACGTCGCGCTAGATTTTCATTAAGTACGAGA 314
Db 1354 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1295
QY 315 GTTAGTCACAAATCCGACGCGCAAGCATTTGCTGTTGTTGAGAACGTCGACCG 374
Db 1294 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1235
QY 375 GATTATAGCCGCGACGAGTACGGAACGTTCCCGCATCGCATGTGTTACGGAAC 434
Db 1234 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1175
QY 435 CTTAAAAATCCGACGACGACGACGATTCGATATGGGTGAATCTGATGAAGA 494
Db 1174 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1115
QY 495 GAAACGTAAACACCTTCTTAACAGTATATAGATTAACATACGACGCGCTTACGCTTC 554
Db 1114 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1055
QY 555 CTC 557
Db 1054 CTC 1052
```

## RESULT 3

US-09-248-796A-6057  
Sequence 6057, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:  
APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
PRIOR FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEO ID NOS: 28208  
SEO ID NO 6057  
LENGTH: 915  
TYPE: DNA  
ORGANISM: Candida albicans  
US-09-248-796A-6057

Query Match 3.8%; Score 40.4; DB 4; Length 915;  
Best Local Similarity 50.5%; Pred. No. 0.011;  
Matches 98; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

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QY 727 GGTCCGTGAATCAGCTCAGTTATTAGCTTTCCGCGCGCGCTTCCGCGCTGCT 786
Db 535 GTTCATGAGATATGAAGATATTGGTAGTTCTTCTGCGAGCTTCTGCTTCCCA 594
QY 787 TAGTCCGCGCTGTTCACAGGCTTCACAGATGCTAGACCACTCTTACAGTTGT 846
Db 595 TTGTCATTTCATTGAATGCTGTATTAAGGTTTACATGATTAAGATTTGT 654
QY 847 CCAAGCAGCGGCTTGTATCCGTTTCAGACGTTACGCTTGAATTTTCAAGACGAG 906
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Db 655 ATTATGATTCGTCTTATCTGTGTGTAAGTCTCTCTGATGATTCCTCAAGAACTTGT 714  
Qy 907 TCGGTATGCGTCC 920  
Db 715 GCTGCTTGGCTGC 728

RESULT 4  
US-08-956-171E-613/C

; Sequence 613, Application US/08956171E  
; Patent No. 6593114  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunesh  
; Gail H. Choi  
; Patrick S. Dillon  
; Craig A. Roosen  
; Steven C. Barash  
; Michael R. Fannon  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5256  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789

## REFERENCE/DOCKET NUMBER: PB248P1

TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439

## INFORMATION FOR SEQ ID NO: 613:

SEQUENCE CHARACTERISTICS:  
LENGTH: 654 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 613:  
US-08-956-171E-613

Query Match 3.2%; Score 34; DB 4; Length 654;  
Best Local Similarity 48.0%; Pred. No. 1.3;  
Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 472 ATGGGGAATCTGTATGAAGAAGAAAGTAAAGCACTTTAAGCTGATATATAGAC 531  
Db 455 ATTACTGCAATTGATTAAGACATAGATAAAGATAGCCAAATATCTGTTAATTGCC 396  
Qy 533 ATAAAGCAGCGGCTTCAAGCTTCCGGTTTAACTGCAATTGCCAGACGACAAAGATC 591  
Db 395 TTAGGATATGACTTTTAAAGGTCATCTGATTCACGACGATTAAGCTACTTCTGTGA 336  
Qy 592 CAACCTCCGCAAGCTTGGCATCATCACTGTGGCTCAGCAACTTTGCCGCAAGGAATG 651  
Db 335 CCACCAACGAAATCCGCGACTAATATATACGCTTAAGAAACAGAGATATACCAACACA 276

Qy 652 TATCCAGATGCGCATTCAT 673  
Db 275 AACGGTCTGGCCTTTGTAT 254

RESULT 5  
US-08-781-986A-613/C

; Sequence 613, Application US/08781986A  
; Patent No. 6732248  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunesh  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

## FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248BP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 613:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 654 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-613

Query Match 3.2%; Score 34; DB 4; Length 654;  
Best Local Similarity 48.0%; Pred. No. 1.3;  
Matches 97; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 472 ATGGGGAATCTGTATGAAGAAGAAAGTAAAGCACTTTAAGCTGATATATAGAC 531  
Db 455 ATTACTGCAATTGATTAAGACATAGATAAAGATAGCCAAATATCTGTTAATTGCC 396  
Qy 533 ATAAAGCAGCGGCTTCAAGCTTCCGGTTTAACTGCAATTGCCAGACGACAAAGATC 591  
Db 395 TTAGGATATGACTTTTAAAGGTCATCTGATTCACGACGATTAAGCTACTTCTGTGA 336  
Qy 592 CAACCTCCGCAAGCTTGGCATCATCACTGTGGCTCAGCAACTTTGCCGCAAGGAATG 651  
Db 335 CCACCAACGAAATCCGCGACTAATATATACGCTTAAGAAACAGAGATATACCAACACA 276  
Qy 652 TATCCAGATGCGCATTCAT 673  
Db 275 AACGGTCTGGCCTTTGTAT 254

RESULT 6  
US-09-949-016-33921

; Sequence 33921, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33921  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-33921

Query Match  
Best Local Similarity 3.1%; Score 33.4; DB 4; Length 601;  
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 29 TTGAGGCAAGATCAACTTAAGAGCCGTTGATCTTAACCATCATCAAGCGGCTCAGAA 88  
DB 100 TTGCTGTCCTTTGGAAAGTCATTTGCACCTGATGACACAAAGGCTCATCTCTGAA 159  
QY 89 AGCTGAACTTCAAGCCTTTCCAGTAATCCCAAGAGAGCTCTGAGCCCAAGCGG 148  
DB 160 TCGTCACTCTGCAGAAAGACAGAAAGAGCCATTCAACACTGGGGCTGGCAGCCAGCAGGG 219  
QY 149 AGCCGGTGATG 159  
DB 220 AGCAGGGCATG 230

RESULT 7  
US-09-949-016-133049  
Sequence 133049, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 133049  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-133049

Query Match  
Best Local Similarity 3.1%; Score 33.4; DB 4; Length 601;  
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 29 TTGAGGCAAGATCAACTTAAGAGCCGTTGATCTTAACCATCATCAAGCGGCTCAGAA 88  
DB 100 TTGCTGTCCTTTGGAAAGTCATTTGCACCTGATGACACAAAGGCTCATCTCTGAA 159  
QY 89 AGCTGAACTTCAAGCCTTTCCAGTAATCCCAAGAGAGCTCTGAGCCCAAGCGG 148  
DB 160 TCGTCACTCTGCAGAAAGACAGAAAGAGCCATTCAACACTGGGGCTGGCAGCCAGCAGGG 219

QY 149 AGCCGGTGATG 159  
DB 220 AGCAGGGCATG 230

RESULT 8  
US-09-949-016-15489/c  
Sequence 15489, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15489  
LENGTH: 34068  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-15489

Query Match  
Best Local Similarity 3.1%; Score 33.4; DB 4; Length 34068;  
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 29 TTGAGGCAAGATCAACTTAAGAGCCGTTGATCTTAACCATCATCAAGCGGCTCAGAA 88  
DB 16953 TTGCTGTCCTTTGGAAAGTCATTTGCACCTGATGACACAAAGGCTCATCTCTGAA 16894  
QY 89 AGCTGAACTTCAAGCCTTTCCAGTAATCCCAAGAGAGCTCTGAGCCCAAGCGG 148  
DB 16893 TCGTCACTCTGCAGAAAGACAGAAAGAGCCATTCAACACTGGGGCTGGCAGCCAGCAGGG 16834  
QY 149 AGCCGGTGATG 159  
DB 16833 AGCAGGGCATG 16823

RESULT 9  
US-09-949-016-12559/c  
Sequence 12559, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12559  
LENGTH: 51711  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-12559

Query Match 3.1%; Score 33.4; DB 4; Length 51711;  
Best Local Similarity 53.4%; Pred. No. 27;  
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 29 TTGACGAGCAAGATCAAACTTAAGAGCCGTTGATCTTAACATCAACGCGCTCAGAA 88  
DB 34596 TTGCTGTCCCTTTGGAAAGTCCATTTGCCACTGATGGACAAAGGCTCATCTCTGTA 34537  
QY 89 ACGTGAAACTTCAAGACCTTTTCCAAAGTAAATCCCACTGATGCTTCAGAGCCCAAGGCGG 148  
DB 34536 TCGTACTCTGCAAGAGCAAGAGGAGCCATTCACACTGGGGCTGGCAGCAGAGG 34477  
QY 149 AGCCGGATGATG 159  
DB 34476 ACCAGGGCATG 34466

RESULT 10  
US-09-252-991A-8192  
Sequence 8192, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 8192  
LENGTH: 2127  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (291)  
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.  
US-09-252-991A-8192

Query Match 3.1%; Score 33; DB 4; Length 2127;  
Best Local Similarity 49.2%; Pred. No. 5.5;  
Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 111 CCAAGTAAATCCACAGTGTCTGAGCCCAAGGCGGAGCGGTGATGCGGCTTTTC 170  
DB 70 CCAAGCTGAACAGCTGAGGCTTATGACAGACGACGCCACCGAGAGGCTTGAGACCC 129  
QY 171 AATGCTTTAGCTCCACCGCTTTCAGACAGACCAACCATTAAGAGACTTGAATAAGA 230  
DB 130 AATACCGGACACCGCATCGCGATTAACAGAACACCTTGAAGGCGGAGCGGACCG 189  
QY 231 CCGTACACGAAAGTTGAAGAGAGGAGAAAGATACGATGCTTCCACGCTGTTC 287  
DB 190 TCGTGTCTGAAAGACTTATCATGCGCGAGAGATCACCACTTGCACCAAGAGCGC 246

RESULT 11  
US-09-252-991A-8112/c  
Sequence 8112, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 8112  
LENGTH: 2874  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (286)  
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.  
US-09-252-991A-8112

Query Match 3.1%; Score 33; DB 4; Length 2874;  
Best Local Similarity 49.2%; Pred. No. 6.5;  
Matches 87; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 111 CCAAGTAAATCCACAGTGTCTGAGCCCAAGGCGGAGCGGTGATGCGGCTTTTC 170  
DB 2487 CCAAGCTGAACAGCTGAGGCTTATGACAGACGACCGCACCGGAGAGGCTTGAGACCC 2428  
QY 171 AATGCTTTAGCTCCACCGCTTTCAGACAGACCAACCATTAAGAGAGCTTGAATAAGA 230  
DB 2427 AATACCGGACACCGCATCGCGATTAACAGAACACCTTGAAGGCGGAGCGGAGCGC 2368  
QY 231 CCGTACACGAAAGTTGAAGAGAGGAGAAAGATACGATGCTTCCACGCTGTTC 287  
DB 2367 TCGTGTCTGAAAGACTTATCATGCGCGAGAGATACCACTTGCACCAAGAGCGC 2311

RESULT 12  
US-09-103-840A-2  
Sequence 2, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 3.1%; Score 32.8; DB 3; Length 4403765;  
Best Local Similarity 59.8%; Pred. No. 2.8e+02;  
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 133 CTGAGCCCAAGAGCGGAGCGGTGATGCGGCTTTTCAATGCTTTAGCTCCACCGTCT 192  
DB 3941480 CTGGCGGACAGAGCGGCGCGGAGGTGCTGTGGCGGGGCGGCGCCATTAACCCACCGGCA 3941539  
QY 193 TCGACAGACCAACCATTAAGAGAGCTTGCAC 224  
DB 3941540 TCGGCGGACACCGGCGGCTGACGCGGCGGACCGGCG 3941571

RESULT 13  
US-09-632-098-5  
Sequence 5, Application US/09632098  
Patent No. 6420154



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Qy 817 ATGGCTAGACCACTCCCTTTACAGTTGTTCCAAGCAGCGGCTTGTATCCGTTTCAGAC 876  
Db 1196 AARGNGNGNGCNTGYTNMSMAAYGCNCNGAYCCNGNNTNCCNGTNCNCNGCNY 1255  
Qy 877 GTTACCGGTTTCAATTTATCAAGAGCAGCGGTTATGCTCCGAGCTCAAGCTCAGGC 936  
Db 1256 TMTGYGNAAYGANTTYGNGARGCNGCNGARGARTGYGYGNCNGNCNGNCARGART 1315  
Qy 937 GTACACACCGGTAGTTCATCGTCAAT 962  
Db 1316 GYMNGAYYTNMTGYTGYGNCAY 1341

Search completed: February 28, 2005, 08:17:49  
Job time : 220.069 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 07:18:54 ; Search time 673.078 Seconds  
(without alignments)  
9428.583 Million cell updates/sec

Title: US-09-938-842a-1034

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
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- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1071	100.0	1071	11	US-09-938-842a-1034
3	448	41.8	460	9	US-09-924-035A-502
4	439	41.0	453	9	US-09-770-444-615
5	228.6	21.3	1847	17	US-10-424-599-109777
6	185	17.3	185	9	US-09-770-696-257
7	183.6	17.1	1090	17	US-10-425-114-8512
8	157.8	14.7	1176	17	US-10-425-114-14614
9	145.2	13.6	1113	17	US-10-424-599-43464
10	144.8	13.5	1616	18	US-10-739-930-3143
11	138	12.9	1594	17	US-10-424-599-63594

12	129	12.0	1519	17	US-10-425-114-14605	Sequence 14605, A
13	129	12.0	1728	10	US-09-934-455-169	Sequence 169, App
14	129	12.0	1728	17	US-10-225-068-165	Sequence 165, App
15	129	12.0	1728	17	US-10-374-780A-219	Sequence 219, App
16	127.4	11.9	671	17	US-10-374-780A-1390	Sequence 1390, App
17	126	11.8	587	18	US-10-021-323-15482	Sequence 15482, A
18	124.6	11.6	1231	17	US-09-934-455-137	Sequence 137, App
19	124.6	11.6	1231	17	US-10-225-068-245	Sequence 245, App
20	124.6	11.6	1231	17	US-10-302-267-61	Sequence 61, App1
21	124.6	11.6	1231	17	US-10-374-780A-2425	Sequence 2425, App
22	124.6	11.6	1231	17	US-10-412-699B-553	Sequence 553, App
23	124.6	11.6	1540	17	US-10-425-114-12989	Sequence 12989, A
24	124.4	11.6	1440	18	US-10-767-795-1247	Sequence 1247, App
25	122.8	11.5	938	18	US-10-767-795-1984	Sequence 1984, App
26	121.6	11.4	1604	15	US-10-295-403-147	Sequence 147, App
27	121.6	11.4	1604	17	US-10-412-699B-551	Sequence 551, App
28	119.8	11.2	587	17	US-10-425-114-30404	Sequence 30404, A
29	119.8	11.2	668	17	US-10-425-114-27401	Sequence 27401, A
30	119.8	11.2	678	18	US-10-425-115-11245	Sequence 11245, A
31	118	11.0	490	10	US-09-770-961-675	Sequence 675, App
32	117.8	11.0	1635	18	US-10-437-963-40920	Sequence 40920, A
33	117.4	11.0	390	11	US-09-732-627A-4287	Sequence 4287, App
34	113.8	10.6	1260	18	US-10-437-963-26590	Sequence 26590, A
35	113.2	10.6	600	18	US-10-767-795-3868	Sequence 3868, App
36	113	10.6	1322	18	US-10-437-963-12388	Sequence 12388, A
37	111.8	10.4	563	18	US-10-767-701-117	Sequence 117, App
38	111.4	10.4	1608	17	US-10-425-114-9860	Sequence 9860, App
39	111.4	10.4	1830	17	US-10-424-599-79271	Sequence 79271, A
40	111.2	10.4	422	9	US-09-770-423-332	Sequence 332, App
41	111.2	10.4	881	17	US-10-425-114-14725	Sequence 14725, A
42	111.2	10.4	1009	15	US-09-934-455-133	Sequence 133, App
43	111.2	10.4	1009	15	US-10-295-403-145	Sequence 145, App
44	111.2	10.4	1009	15	US-10-278-536-203	Sequence 203, App
45	111.2	10.4	1009	17	US-10-225-068-135	Sequence 135, App

## ALIGNMENTS

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RESULT 1
US-09-938-842a-1034
; Sequence 1034, Application US/0993842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1034
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842a-1034
Query Match 100.0%; Score 1071; DB 9; Length 1071;
Best local similarity 100.0%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGGCGACATTTCAGAGCTTGAAGAGTTGCAGGCAAGATCAAACTCTTAAGACCGTT 60
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QY 61 GATCTAACCATCATCAACGGGCTCAGAAAGCTGAAATTTCAAGACTTTCCAGTAAT 120  
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QY 121 CCCACAGTAGTCTCGAGCCCAAGGGGAGCGGTGATCCGTGCTTTCAATGCTTTA 180  
Db 121 CCCACAGTAGTCTCGAGCCCAAGGGGAGCGGTGATCCGTGCTTTCAATGCTTTA 180  
QY 181 GCTCCACCGCTTTCGACAGGACCAATTTGAAGAAGGCTTCACTPAAGACCTGACACG 240  
Db 181 GCTCCACCGCTTTCGACAGGACCAATTTGAAGAAGGCTTCACTPAAGACCTGACACG 240  
QY 241 AAGGTTGAAGAAAGAGGAGAAAGATACGATGCTGCGACGCTGCGGCTGATTTT 300  
Db 241 AAGGTTGAAGAAAGAGGAGAAAGATACGATGCTGCGACGCTGCGGCTGATTTT 300  
QY 301 CAATTAACTCGAGAGTAGTCACAAAATCCGACGCGGAAACGATTCGGTGGTTGGAG 360  
Db 301 CAATTAACTCGAGAGTAGTCACAAAATCCGACGCGGAAACGATTCGGTGGTTGGAG 360  
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QY 721 ATCCGTGCTCGGTGATCAAGCTTCAAGTATTTAGCTTTTCCGCGCGCTGCTGCGCG 780  
Db 721 ATCCGTGCTCGGTGATCAAGCTTCAAGTATTTAGCTTTTCCGCGCGCTGCTGCGCG 780  
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QY 901 GCGAGCTCGGTTTATGCTTCGAGCTCAAGCTCAAGGCTTCCAGAGCTTCAAGTATTAAGA 960  
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QY 1021 GAGCTTCAACAGTTCATGAGACCAACAGACGAGCTCAATGCAACCACTGA 1071  
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RESULT 2  
US-09-938-842A-1034  
; Sequence 1034, Application US/09938842A

; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Hong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 1034  
; LENGTH: 1071  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1034

Query Match 100.0%; Score 1071; DB 11; Length 1071;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1071; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGGCGACAAATTCAGAGCTTGAAGAGTTGAGAGCAAGATCAAACTCTAAGAGCGCTT 60  
QY 61 GATCTAACCATCATCAACGGGCTCAGAAAGCTGAAATTTCAAGACTTTCCAGTAAT 120  
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QY 481 AATCTGATGAGAAAGAAACGTAAAGACCTTCAACAGTGAATATAGACATTAAGGAC 540  
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QY 661 TGGGCTATTCATCAAAACGCAATGATTCGACGAGCTTCTTCTTGAATTCGACAA 720

Db 661 TGGGCTATTCATCAAAACCAATGATTCGACGCTCGAGCTTCTCTTGATTCACAA 720  
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Qy 961 ATTGCAACAACAGCAGCAGCAGCTTCTCCCTAGAGATATACAGAAACAA 1020  
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## RESULT 3

US-09-924-035A-502/c  
Sequence 502, Application US/09924035A  
Patent No. US20020142319A1  
GENERAL INFORMATION:  
APPLICANT: Glach, Jirn  
TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
FILE REFERENCE: 2011US  
CURRENT APPLICATION NUMBER: US/09/924,035A  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: US 60/148,784  
NUMBER OF SEQ ID NOS: 900  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 502  
LENGTH: 460  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(460)  
OTHER INFORMATION: n = A,T,C or G  
US-09-924-035A-502

Query Match 41.8%; Score 448; DB 9; Length 460;  
Best Local Similarity 99.6%; Pred. No. 6e-143; Indels 1; Gaps 1;  
Matches 459; Conservative 0; Mismatches 1;

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Db 460 GCAAGCTGCGATCATCATCTGTGCTCAGCAACTTTCGCGCAAGATGATTCGAT 401  
Qy 660 GTGGGCTATTCATCAAAAGCAATGATTCGAGCGGTGAGCTTTTCTTGAATTCACA 719  
Db 400 GTGGGCTATTCATCAAAAGCAATGATTCGAGCGGTGAGCTTTTCTTGAATTCACA 341  
Qy 720 AATGCTGTCGTCGATCAAGCTTCATGATTAAGCTTTTCCGCGCGCTGCTTCGCC 779  
Db 340 AATGCTGTCGTCGATCAAGCTTCATGATTAAGCTTTTCCGCGCGCTGCTTCGCC 282  
Qy 780 GTGCTTAAAGTGGCGGCTGCTTCACAGGCTTCACAGATGGCTAGACCACTCTTAC 839  
Db 281 GTGCTTAAAGTGGCGGCTGCTTCACAGGCTTCACAGATGGCTAGACCACTCTTAC 222

Qy 840 AGTGTTCACAGCAGCGGCTTGTATCCGTTTCAGAGCTTACGCGGTGATTTACAG 899  
Db 221 AGTGTTCACAGCAGCGGCTTGTATCCGTTTCAGAGCTTACGCGGTGATTTACAG 162  
Qy 900 AGCGAGCTGCTTATGCTTCGAGCTCAAGCTCAGCGGTAAACCGGTATGCTATGCTC 959  
Db 161 AGCGAGCTGCTTATGCTTCGAGCTCAAGCTCAGCGGTAAACCGGTATGCTATGCTC 102  
Qy 960 AATTGCAACAACAGCAGCAGCAGCTTCTCCCTAGAGATATACAGAAACAA 1019  
Db 101 AATTGCAACAACAGCAGCAGCAGCTTCTCCCTAGAGATATACAGAAACAA 42  
Qy 1020 AGAGCTTACCACTTATGAGCAGCAGCAGCTTCTCCCTAGAGATATACAGAAACAA 1060  
Db 41 AGAGCTTACCACTTATGAGCAGCAGCAGCTTCTCCCTAGAGATATACAGAAACAA 1

## RESULT 4

US-09-770-444-615/c  
Sequence 615, Application US/09770444  
Patent No. US2002023280A1  
GENERAL INFORMATION:  
APPLICANT: Gorlach, Jörn  
APPLICANT: An, Yong-Qiang  
APPLICANT: Hamilton, Carol M.  
APPLICANT: Price, Jennifer L.  
APPLICANT: Raines, Tracy M.  
APPLICANT: Yu, Yang  
APPLICANT: Rameaka, Joshua G.  
APPLICANT: Page, Amy  
APPLICANT: Matthew, Abraham V.  
APPLICANT: Ledford, Brooke L.  
APPLICANT: Moesner, Jeffrey P.  
APPLICANT: Haas, William David  
APPLICANT: Garcia, Carlos A.  
APPLICANT: Kricker, Maja  
APPLICANT: Slader, Ted  
APPLICANT: Davis, Keith R.  
APPLICANT: Allen, Keith  
APPLICANT: Hoffman, Neil  
APPLICANT: Hurdan, Patrick  
TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
FILE REFERENCE: 2027 (PARA-016PRV)  
CURRENT APPLICATION NUMBER: US/09/770,444  
PRIOR FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 60/178,502  
NUMBER OF SEQ ID NOS: 999  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 615  
LENGTH: 453  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(453)  
OTHER INFORMATION: n = A,T,C or G  
US-09-770-444-615

Query Match 41.0%; Score 439; DB 9; Length 453;  
Best Local Similarity 99.1%; Pred. No. 7.5e-140; Indels 1; Gaps 1;  
Matches 450; Conservative 0; Mismatches 3;

Qy 607 CTGGCATCATCAGCTGTGCTCAGCAACTTTCGCGCAAGATGATTCGATGAGCT 666  
Db 453 CTGGCATCATCAGCTGTGCTCAGCAACTTTCGCGCAAGATGATTCGATGAGCT 394  
Qy 667 AATTCATCAAAAGCAATGATTCGAGCGGTGAGCTTTCTTGAATTCACAAATGCT 726  
Db 393 AATTCATCAAAAGCAATGATTCGAGCGGTGAGCTTTCTTGAATTCACAAATGCT 334  
Qy 727 GGTGCTGCAATCAAGCTTCATGATTAAGCTTTCCGCGCGCTGCTGCGCTGCT 786

```

RESULT 5
US-10-424-599-109777
; Sequence 109777, Application US/10424599
; Publication No. US20040031072A1
GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5323)B
; CURRENT APPLICATION NUMBER: US/10/424.599
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 109777
; LENGTH: 1847
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_70141C.1
US-10-424-599-109777

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	Query Match	Similarity	21.38;	Score 228.6;	DB 17;	Length 1847;
	st Local	Similarity	62.7%;	Pred. No. 5e-67;		
	atches 398;	Conservative	0;	Mismatches 219;	Indels 18;	Gaps 2
QY	136	GAGCCCAAGGCGGAGCCGGTGAATGCCGTGTTTCAATATGTTTAACTCCACCGCTTTCG	195			
Db	329	GTGACACGTGCCGGCGGGAGATGTCATATGTCACATGTCACAAAGCTCTGCGCCAGGCCCAAGCC	388			
QY	196	ACAGACCAACCATTTGAAGAGAGCTTCGACTTAAGACGGTCAACAGAAAGTTGAAGAGACA	255			
Db	389	CAGGCCCAACCAAAAAGGGGGCTCTCAACAAAGACGGCAACAAAGTAGAGGGGGCA	448			
QY	256	GGGAGAAAGGATAGCGATGCTTCGCAACGTCGCGGCTAGATTTTTCAATTAATCTGAGAG	315			
Db	449	GGCAGAAAGATTCGAATGCCCCGCCACGTCGTGCGCGAGAGATCTTCAAGCTGACCCGAAG	508			
QY	316	TTAGTGTCACAAAATCCGACGGCGGAAACGATTTGGTGTGTTTGAGAGACGCTAGCGCGG	375			
Db	509	CTGGGTCAATTAATCCGACGGGAAACCAATCGGTGGTCTCTCGAGACCGCGAGGCCGCC	568			
QY	376	ATTATAGCCCGCAACGGGTATCGGAAACGGTTCGCCCATGTCCATGTCTTAAACGAAAC	435			
Db	569	ATCATGCGCGCACCGGACCGGACAGTCCCCGCCATGCGCATGTTCGGTCAATGGAACG	628			
QY	436	TTAAAATCCGACGACGACCAACGCTGATTCGATATGGGTGAATAATCTGATGAAGAG	495			

Db 629 TTTAAAGATTCGCACCACTTCACTTCGATCAAGAACCCGAGAGCCGCCCGAGAGGAG 688

Qy 496 AAAGTAAACGACCTTTCTTAACAGTAGTATATAGACATTA---GGAGCCGCTTTCAGCT 552

Db 669 AAGGCAAAACGACCCCGGAATAGCGCTTCGTGAGCATTAACGGCGCGCGCTTTCGCTC 748

Qy 553 TCTCCGGTTTAGCTCCAAATGGCACAGAGAAAGATTCCACTCCGCAAGCTTCGCA 612

Db 749 TCGCCCGGGCTCGCAGAGCTCTATTAATTAATTAATTAACAAACGAGCAAGCAGATG 808

Qy 613 TCATCCACTTGGCTCAGCACTTC-----TGCAGCAAGATATGATCCG 657

Db 809 ACGCAACAGATGGCAATTCGCGAACAATACAGCAATTCGTTGCGCGCAAGAAATGTTCC 868

Qy 658 ATGTGGCTATTTCCATCAAAACGCAATGATTCGACGCGGAGGTTTCTCTTGATTCGA 717

Db 869 GTGTGGGCAATCCCTTCAAAACGCGGTGCTTCGGCTCAGAGACTTTTGTGGTCTCT 928

Qy 718 CAAATCGTGTGCGGCGAATCAGCCATCATTT 752

Db 929 CAAACGGCGCTTTCAGATCAACCTCAAGTTT 963

```

RESULT 6
US-09-770-696-257
; Sequence 257, Application US/09770696
; Patent No. US2001004940A1
GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Ochang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke U.
; APPLICANT: Moesener, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kriker, Maja
; APPLICANT: Slader, Red
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hubban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2031US (PARA-020PRV)
CURRENT APPLICATION NUMBER: US/09770,696
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,278
NUMBER OF SEQ ID NOS: 911
SOFTWARE: FASESQ for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-696-257

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Query Match	17.3%	Score 185	DB 9	Length 185
Best Local Similarity	100.0%	Pred. No. 1.3e-52		
Matches 185	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	35	GCMAAGATCAAACTTGAAGCCGCTGATCTAATCAATCATCAACGGCGTCCAGAAACGTCG		94
Db	1	GCAAGATCAAACTTGAAGCCGCTGATCTAATCAATCAACGGCGTCCAGAAACGTCG		60
QY	95	AAACTTCAAGACCTTTCCAGTAATCCACAGTAGTGTGCGAGGCCAAGAGCGGAGCCGCG		154
Db	61	AAACTTCAAGACCTTTCCAGTAATCCACAGTAGTGTGCGAGGCCAAGAGCGGAGCCGCG		120

QY 155 TGATGCCGTCGTTTCAATGCTTAACTCAACCGCTTCGACAGACCAACCATTTGAAGA 214  
DB 121 TGATGCCGTCGTTTCAATGCTTAACTCAACCGCTTCGACAGACCAACCATTTGAAGA 180  
QY 215 GAGCT 219  
DB 181 GAGCT 185

RESULT 7  
US-10-425-114-8512  
; Sequence 8512, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingtong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack B  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 8512  
; LENGTH: 1090  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700756889\_FLI  
US-10-425-114-8512

Query Match 17.1%; Score 183.6; DB 17; Length 1090;  
Best Local Similarity 63.7%; Pred. No. 1,2e-51;  
Matches 320; Conservative 0; Mismatches 164; Indels 18; Gaps 2;

QY 269 GATGCTCTGCAAGTGTGCGGCTAGATTTTCAATTAACGAGATTAGTCACAAA 328  
DB 1 GAATGCTCTGCAAGTGTGCGGCTAGATTTTCAATTAACGAGATTAGTCACAAA 60  
QY 329 CCGAGCGGCAAAAGTGTGCTGTTTGAAGAACGCTACCGGAGATTAGCCGCA 388  
DB 61 CCGAGCGGCAAAAGTGTGCTGTTTGAAGAACGCTACCGGAGATTAGCCGCA 120  
QY 389 CCGGTAACGGGAACGTTTCCGCGCATGCGCATGCGTTAAAGGAACCTTAAATCCGA 448  
DB 121 CCGGTAACGGGAACGTTTCCGCGCATGCGCATGCGTTAAAGGAACCTTAAATCCGA 180  
QY 449 CGACGACGAAGCGTATGTAATGAGTGAATGTAAGAAAGAAACGTAAGAC 508  
DB 181 CAACCTCACTTCGATCAAGAACCGGAGAGCCGCCGAGAGAAAGAACGCAACGAC 240  
QY 509 CTTTCAACGTAAGTATAGACATTA---GGAGCGCGTTTCAAGTTCTCCGCTTGA 565  
DB 241 CCGGTAATGCGCTTACGTAACGTAAGCGGCGCGCTTTCGCTGCGCGCGGCTG 300  
QY 566 CTCGAATTCGACGACGACGAACGATCCGCACTCGGCACTGCGATCATCCTGCTG 625  
DB 301 CAAGCTATTTATTAATTAACCAAAACGACGAACGACGATGACGAACGATG 360  
QY 626 CTCAGCACTTC-----TCCCGCAAGAAATGATCCGATGCGGCTATTC 670  
DB 361 CAATTCGCAATACAGCAATTCGCTGCGGCAAGAAATGTTCCGATGCGGCTATTC 420  
QY 671 CATCAAAACCAATGATTCGAGCGTGGAGCTTTCTTGAATTCGCAAAATGCGTGGTC 730  
DB 421 CTTCAAAACCGCTGCTGCGGCTGCAAGAGCTTTTGTGTTCTCAAAACGCGCTGCT 480  
QY 731 CGTCGAATCAGCTCAGTTATT 752

DB 481 TTCAGATCAACCTCAGTTT 502

RESULT 8  
US-10-425-114-14614  
; Sequence 14614, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingtong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack B  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 14614  
; LENGTH: 1176  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB23-065-D10\_FLI  
US-10-425-114-14614

Query Match 14.7%; Score 157.8; DB 17; Length 1176;  
Best Local Similarity 75.9%; Pred. No. 9.3e-43;  
Matches 195; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 195 GACAGATCCACCATGGAAGAGCTTCGACTTAAGACCGTCAACGAGGTTGAAGAG 254  
DB 278 GACTAAACCGCTCCGAAAGAGACGACTTAAGACCGTCAACGAGGTTGAAGAG 337  
QY 255 AGGAGAAAGATACGATGCTGCGCAGTGTGCGGCTAGATTTTCAATTAACGAG 314  
DB 338 AGGTGAGAGATCCGAATGCCGCGGTTGCGCTGCTGCTTCAATTAACGAG 397  
QY 315 GTTAGTCACAAAATCGACGCGGAAACGATTCGATGTTTGAAGAACGCTGACCGGC 374  
DB 398 ACTTGTCACAAATCGACGCGGAAACGATTCGATGTTTGAAGAACGCTGACCGGC 457  
QY 375 GATTATAGCCGCAAGGTAAGGAAACGTTCCCGCATGCGATGCTGTTAAAGGAAC 434  
DB 458 GATTAATTGAAGCAACCGAAACGTAACGCTATGCTGTAACGTTAAAGGAAC 517  
QY 435 CTTAAAAATCCGACGA 451  
DB 518 TTTAAAAATCCGACGA 534

RESULT 9  
US-10-424-599-43464  
; Sequence 43464, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K  
; APPLICANT: Tabaska, Jack B  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5323)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 43464  
; LENGTH: 1113  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:

NAME/KEY: unsure  
LOCATION: (1)..(113)  
OTHER INFORMATION: unsure at all n locations  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_139247C.1  
US-10-424-599-43464

Query Match 13.6%; Score 145.2; DB 17; Length 1113;  
Best Local Similarity 64.8%; Pred. No. 2e-38;  
Matches 232; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 221 CGACTAAGACCGCTCAGAGAGTTGAAGAGAGAGAGAGATACGATGCTGCGCA 280  
DB 635 CGTCCAGAGATCGCACACGAGGTGAGGCTGTGGCCGCGAGATCAGATGCGCGCA 694  
QY 281 CGTGTGCGGCTAGATTTCATTAACTCAGAGATTAGTCAAAATCCGCGCGCA 340  
DB 695 CATGCCGCGGAGATCTTCCAGCTGACCCGGAACTGGACACAAAGTCCGAGGGA 754  
QY 341 CGATTCCGCTGTTTGGAGAAAGCTGAGCCGCGCATTAATAGCCGCAAGGTAACG 400  
DB 755 CAATCCGCTGTGCTGGAGCAAGCTGAGCCGCAATCATCGAGGCGCACCGGCA 814  
QY 401 CGATTCCGCGCATCGCATGATGCTGTTAAAGGAACTTAAATCCGCGAGAGCAAG 460  
DB 815 CATCCCGCGCATCCCGCTGCTGCTGCGGCGGCACTCAAGATTCGACATCTCGGCA 874  
QY 461 CTGATTCTGATATGAGTGAATAATCTGATGAAGAGAGAGAGAGAGATCAACAGT 520  
DB 875 CAAGACCGGAG 934  
QY 521 AGTATATGACATAGCG---ACGCGCTTCAAGCTTCTCCGCTTACCTCAATTCG 575  
DB 935 AATTATGACGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 992

RESULT 10  
US-10-739-930-3143  
Sequence 3143, Application US/10739930  
Publication No. US20040216190A1  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
TITLE OF INVENTION: NOCLETIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
FILE REFERENCE: 38-21(53377)B  
CURRENT APPLICATION NUMBER: US/10/739, 930  
CURRENT FILING DATE: 2003-12-18  
NUMBER OF SEQ ID NOS: 11088  
LENGTH: 1616  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER131780\_1  
US-10-739-930-3143

Query Match 13.5%; Score 144.8; DB 18; Length 1616;  
Best Local Similarity 63.5%; Pred. No. 3.4e-38;  
Matches 240; Conservative 0; Mismatches 132; Indels 6; Gaps 1;

QY 202 CCACCATTTGAAGAGAGCTTGAATTAAGACCTCAGAGAGTTGAAGAGAGAGAG 261  
DB 399 CTTCCAG 458  
QY 262 AGGATACGATGCTGCGACGCTGAGGCTAGGATTTTCAATTAATCTGAGAGTTAGT 321  
DB 459 AGGATCGGATATCCCGACCTGCGCGCGCGGATCTTCCAGCTGACCGGAGAGCTCG 518  
QY 322 CAGAAATCCGAGCGGAGAGAGATTCGCTGCTGTTGAGAGAGCTGAGCGCGGATTA 381  
DB 519 CACAAATCCGAGCGGAGAGAGATTCGCTGCTGTTGAGAGAGCGGAGCGGATTA 578  
QY 382 GCGGACGAGGAG 441

DB 579 GAGGCGACCGGACCGGATGATGCTGATGATGATGATGATGATGATGATGATGATGAT 638  
QY 442 ATCCGAG 501  
DB 639 ATCCGAG 698  
QY 502 AAAG 555  
DB 699 AAAG 758  
QY 556 TCCGCTTACCTCAATT 573  
DB 759 TCCGCTTACCTCAATT 776

RESULT 11  
US-10-424-599-63594  
Sequence 63594, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 63594  
LENGTH: 1594  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_28439C.1  
US-10-424-599-63594

Query Match 12.9%; Score 138; DB 17; Length 1594;  
Best Local Similarity 64.6%; Pred. No. 7.3e-36;  
Matches 248; Conservative 0; Mismatches 115; Indels 21; Gaps 2;

QY 211 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 270  
DB 369 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 428  
QY 271 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330  
DB 429 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488  
QY 331 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390  
DB 489 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548  
QY 391 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450  
DB 549 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608  
QY 451 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 501  
DB 609 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668  
QY 502 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 549  
DB 669 AAGAGAGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728  
QY 550 GCTTCTCCGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 573  
DB 729 GCTTCTCCGCTTCACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 752

RESULT 12

US-10-425-114-14605  
; Sequence 14605, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 14605  
; LENGTH: 1519  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB23-047-E8\_FLI  
US-10-425-114-14605  
Query Match 12.0%; Score 129; DB 17; Length 1519;  
Best Local Similarity 71.0%; Pred. No. 8.9e-33;  
Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
QY 189 GTCTTCGACAGGACCACTTGAAGAGAGCTTGAATAAGACCGTCACAGAGGTTGA 248  
DB 68 GGCAGCTAAAAGCCACCGTTGAAACGAGCTGACGAAAGACCGACACAGAAAGTAGA 127  
QY 249 AGGAAGAGGAGAGAGATACGATGCTTCCACAGTGTGGGCTAGATTTTCAATTAC 308  
DB 128 CGGAAGAGGAGAGAGATACGATGCTTCCACAGTGTGGGCTAGATTTTCAATTAC 187  
QY 309 TCGAGAGTTAGGTCAAAATCCGACGCGGAAAGATTCGGTGTGTTGAGAGAGCTGA 368  
DB 188 GCGAAGCTAGTCAATTAATCCGACGCTGAGACATAGAGTGGCTTTCAACAGCTGA 247  
QY 369 GCGGCGATTATAGCCGCGACGCGGTAACGCGTTCGCCGATCGCCATGTCGGTTAA 428  
DB 248 ACCATCTGTAATCGCGCGACCGGAAACCGGAACATCCCGGGAATTCACCTTTTAA 307  
QY 429 C 429  
DB 308 C 308  
RESULT 13  
US-09-934-455-169  
; Sequence 169, Application US/09934455  
; Publication No. US20030121070A1  
; GENERAL INFORMATION:  
; APPLICANT: Adam, Luc  
; APPLICANT: Creelman, Robert  
; APPLICANT: Dubell, Arnold  
; APPLICANT: Heard, Jacqueline  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Kiedde, James  
; APPLICANT: Piligrim, Marsha  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Reuber, Lynne  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Pineda, Omaira  
; TITLE OF INVENTION: Genes for Modifying Plant Traits IV  
; FILE REFERENCE: MBI-0025  
; CURRENT APPLICATION NUMBER: US/09/934,455  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227439  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: MBI-0022

PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: MBI-0023  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 516  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 169  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (106)..(1575)  
; OTHER INFORMATION: G1064  
US-09-934-455-169  
Query Match 12.0%; Score 129; DB 10; Length 1728;  
Best Local Similarity 71.0%; Pred. No. 9.6e-33;  
Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
QY 189 GTCTTCGACAGGACCACTTGAAGAGAGCTTGAATAAGACCGTCACAGAGGTTGA 248  
DB 420 GGCAGCTAAAAGCCACCGTTGAAACGAGCTGACGAAAGACCGACACAGAAAGTAGA 479  
QY 249 AGGAAGAGGAGAGAGATACGATGCTTCCACAGTGTGGGCTAGATTTTCAATTAC 308  
DB 480 CGGAAGAGGAGAGAGATACGATGCTTCCACAGTGTGGGCTAGATTTTCAATTAC 539  
QY 309 TCGAGAGTTAGGTCAAAATCCGACGCGGAAAGATTCGGTGTGTTGAGAGAGCTGA 368  
DB 540 GCGAAGCTAGTCAATTAATCCGACGCTGAGACATAGAGTGGCTTTCAACAGCTGA 599  
QY 369 GCGGCGATTATAGCCGCGACGCGGTAACGCGTTCGCCGATCGCCATGTCGGTTAA 428  
DB 600 ACCATCTGTAATCGCGCGACCGGAAACCGGAACATCCCGGGAATTCACCTTTTAA 659  
QY 429 C 429  
DB 660 C 660  
RESULT 14  
US-10-225-068-165  
; Sequence 165, Application US/10225068  
; Publication No. US20030217383A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: Reuber, T. Lynne  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Heard, Jacqueline E.  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Adam, Luc J.  
; APPLICANT: Dubell, Arnold T.  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Pineda, Omaira  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Brown, Pierre E.  
; TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND  
; TITLE OF INVENTION: POLYPEPTIDES IN PLANTS  
; FILE REFERENCE: 51442002040  
; CURRENT APPLICATION NUMBER: US/10/225,068  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 60/310,847  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/336,049  
; PRIOR FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/338,692  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: 10/171,468  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 165  
; LENGTH: 1728

TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (106)...(1575)  
US-10-225-068-165

Query Match 12.0%; Score 129; DB 17; Length 1728;  
Best Local Similarity 71.0%; Pred. No. 9.6e-33;  
Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 189 GTCTTGAAGAGACCACTTGAAGAGCTTCACTAAAGCCCTCACAGAAAGTTGA 248  
DB 420 GGCAGCTAAAGACCACTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGTTGA 479  
QY 249 AGGAAGAGGAGAGAGATACGATGCTGCGACGATGCTGCGATGCTTCAATTAC 308  
DB 480 CGGAAGAGGAGAGATACGATGCTGCGACGATGCTTCAAGTTTCAAGTTAC 539  
QY 309 TCGAGAGTTAGTCACTAAATCCGACGCGAAACGATTCGTTGTTGAGAAAGCTGA 368  
DB 540 GCGAAGAGTAAAGTCACTAAATCCGACGCGATGCTTCAAGTTTCAAGTTAC 599  
QY 369 GCCGCGATTATAGCCGCGACGCGATGCGGAAACGATTCGCGCATCGCATGCTTAA 428  
DB 600 ACCATCTGTAATGCGCGCACCGGAAACGGAACCAATCCGCGAATTTCACTTTTAA 659  
QY 429 C 429  
DB 660 C 660

## RESULT 15

US-10-374-780A-219  
Sequence 219, Application US/10374780A  
Publication No. US2004001927A1  
GENERAL INFORMATION:  
APPLICANT: Sherman, Bradley K  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Heard, Jacqueline E  
APPLICANT: Haake, Volker  
APPLICANT: Creelman, Robert A  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Adam, Luc J  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddie, James  
APPLICANT: Brown, Pierre E  
APPLICANT: Pilgrim, Marsha L  
APPLICANT: Duddell III, Arnold T  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
FILE REFERENCE: MBI-0047 CIP  
CURRENT APPLICATION NUMBER: US/10/374,780A  
CURRENT FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: 09/837,944  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/934,455  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
PRIOR APPLICATION NUMBER: 10/225,066  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,067  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,068

PRIOR FILING DATE: 2002-08-09  
NUMBER OF SEQ ID NOS: 2906  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 219  
LENGTH: 1728  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
OTHER INFORMATION: G1064  
US-10-374-780A-219

Query Match 12.0%; Score 129; DB 17; Length 1728;  
Best Local Similarity 71.0%; Pred. No. 9.6e-33;  
Matches 171; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 189 GTCTTGAAGAGACCACTTGAAGAGCTTCACTAAAGCCCTCACAGAAAGTTGA 248  
DB 420 GGCAGCTAAAGACCACTTGAAGAGCTTGAAGAGCTTGAAGAGCTTGAAGAGTTGA 479  
QY 249 AGGAAGAGGAGAGAGATACGATGCTGCGACGATGCTGCGATGCTTCAATTAC 308  
DB 480 CGGAAGAGGAGAGATACGATGCTGCGACGATGCTTCAAGTTTCAAGTTAC 539  
QY 309 TCGAGAGTTAGTCACTAAATCCGACGCGAAACGATTCGTTGTTGAGAAAGCTGA 368  
DB 540 GCGAAGAGTAAAGTCACTAAATCCGACGCGATGCTTCAAGTTTCAAGTTAC 599  
QY 369 GCCGCGATTATAGCCGCGACGCGATGCGGAAACGATTCGCGCATCGCATGCTTAA 428  
DB 600 ACCATCTGTAATGCGCGCACCGGAAACGGAACCAATCCGCGAATTTCACTTTTAA 659  
QY 429 C 429  
DB 660 C 660

Search completed: February 28, 2005, 12:00:32  
Job time : 676.078 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 01:43:47 ; Search time 328.931 Seconds  
(without alignments)  
8342.279 Million cell updates/sec

Title: US-09-938-842a-3729

Perfect score: 1677  
Sequence: 1 ggttagcgttactatg.....ttctctcagctatctta 1677

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues  
number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/6C COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/6D COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59.8	3.6	1141	US-09-806-708B-22	Sequence 22, Appl
2	46.4	2.8	7218	US-08-232-463-14	Sequence 14, Appl
3	45	2.7	1141	US-09-806-708B-22	Sequence 22, Appl
4	44.4	2.6	832	US-09-621-976-2813	Sequence 2813, Ap
5	43.4	2.6	640681	US-09-790-988-1	Sequence 1, Appl
6	43.2	2.6	263693	US-09-949-016-12386	Sequence 12386, A
7	43.2	2.6	263693	US-09-949-016-16915	Sequence 16915, A
8	42.4	2.5	222452	US-09-949-016-12968	Sequence 12968, A
9	42.2	2.5	1666	US-08-076-090-1	Sequence 1, Appl
10	42.2	2.5	1666	PCT-US94-06661-1	Sequence 1, Appl
11	42.2	2.5	2500	US-08-550-715-10	Sequence 10, Appl
12	42.2	2.5	3385	US-09-411-449-3	Sequence 3, Appl
13	42.2	2.5	3385	US-09-710-279-3535	Sequence 3535, Ap
14	42.2	2.5	3496	US-09-411-449-1	Sequence 1, Appl
15	42.2	2.5	3496	US-09-411-449-4	Sequence 4, Appl
16	42.2	2.5	3916	US-09-411-449-2	Sequence 2, Appl
17	42.2	2.5	3916	US-09-949-016-13419	Sequence 13419, A
18	42.2	2.5	5606	US-09-949-016-13419	Sequence 13419, A
19	42	2.5	1440	PCT-US96-09430-7	Sequence 2589, Ap
20	41.2	2.5	601	US-09-107-532A-2589	Sequence 67615, A
21	41.2	2.5	601	US-09-949-016-67615	Sequence 67615, A
22	41.2	2.5	640681	US-09-790-988-1	Sequence 1, Appl
23	40.8	2.4	33411	US-09-949-016-15201	Sequence 15201, A
24	40.8	2.4	118382	US-09-949-016-15996	Sequence 15996, A
25	40.2	2.4	118382	US-09-949-016-15996	Sequence 15996, A
26	40.2	2.4	104428	US-09-949-016-12737	Sequence 12737, A
27	40.2	2.4	104429	US-09-949-016-13814	Sequence 13814, A

C	28	40	2.4	163181	4	US-09-949-016-13730	Sequence 13730, A
C	29	40	2.4	387902	4	US-09-949-016-14543	Sequence 14543, A
C	30	40	2.4	421883	4	US-09-949-016-12557	Sequence 12557, A
C	31	39.8	2.4	25227	4	US-09-949-016-11847	Sequence 11847, A
C	32	39.8	2.4	25227	4	US-09-949-016-14863	Sequence 14863, A
C	33	39.6	2.4	601	4	US-09-949-016-67616	Sequence 67616, A
C	34	39.6	2.4	837	3	US-08-998-416-288	Sequence 288, Ap
C	35	39.6	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl
C	36	39.4	2.3	22871	4	US-09-949-016-15689	Sequence 15689, A
C	37	39.4	2.3	22871	4	US-09-949-016-15689	Sequence 15689, A
C	38	39.2	2.3	601	4	US-09-949-016-150645	Sequence 150645, A
C	39	39.2	2.3	601	4	US-09-949-016-150646	Sequence 150646, A
C	40	39.2	2.3	811	4	US-09-270-767-5788	Sequence 5788, Ap
C	41	39.2	2.3	811	4	US-09-270-767-21070	Sequence 21070, A
C	42	39.2	2.3	77586	4	US-09-949-016-13220	Sequence 13220, A
C	43	39.2	2.3	77586	4	US-09-949-016-13221	Sequence 13221, A
C	44	39.2	2.3	283538	4	US-09-949-016-13506	Sequence 13506, A
C	45	39.2	2.3	294836	4	US-09-949-016-15974	Sequence 15974, A

## ALIGNMENTS

RESULT 1  
US-09-806-708B-22/c  
Sequence 22, 6784342  
Patent No. 6784342  
GENERAL INFORMATION:  
APPLICANT: The University of British Columbia  
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants  
FILE REFERENCE: 4810-58741  
CURRENT APPLICATION NUMBER: US/09/806,708B  
PRIOR FILING DATE: 2001-04-03  
PRIOR APPLICATION NUMBER: US 60/147,133  
PRIOR FILING DATE: 1999-08-04  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 22  
LENGTH: 1141  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (1) - (1141)  
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters  
US-09-806-708B-22

Query Match 3.6%; Score 59.8; DB 4; Length 1141;  
Best Local Similarity 10.5%; Pred. No. 5.8e-06;  
Matches 85; Conservative 299; Mismatches 422; Indels 3; Gaps 1;

855 TCGATTACTTGAATCTGATTTCTAGTGGCTTGTGATGTTTAATTCGAGATTGACAG 914  
1002 TNNAAVYATFWAAVAAAKWAMWGAAGNNRMVGAAGKGCMAAATWBMWADTAGKXC 943  
915 TACACAGTACATAGTATGCGTATATGATGTGACCGGTTTAATCAAGAGCAGCAT 974  
942 NNNNNNTTDDVRRMKAONNNNNNAVWYATCYNRAATNNKMAATTHWKKWGHGHSKRTRH 883  
975 AGAGAGATTTGGAATCTCGAAGAAGATTTATTCACATGACATTAATGCTTTTGGT 1034  
882 HRTTCRTTNN 823  
1035 GCGCAGCCTTGTGACCTAATTAATGCGGTCAACCCAGTATGCGCTTACAGCTTT 1094  
822 KISWCKNN 763  
1095 TCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1152  
762 TWCCTTNN 703  
1153 -TCCAACCATAGAAAGTTAAATTTGATCAGCATGGAATTTTGTACAAAGCTAGTGA 1211





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/ Sequence 12386, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12386
/ LENGTH: 263693
/ TYPE: DNA
/ ORGANISM: Human
/ US-949-016-12386
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Query Match
Best Local Similarity 46.9%; Pred. No. 1.5; Length 263693;
Matches 135; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
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QY 1127 AACCATTAATAATTATTAATAATCTTCCACCATAGAAAAGTAATTTGATCAGCAT 1186
Db 177419 AAGCCATTAATAACCTTTCTAATCTCTAGATATTTGAAAACCTTTATGTTCTTCTGTC
QY 1187 GGAATTTTGTACAAAGTAGTATTTGATTTGAGAGTGTACTAGTAAGTATAC 1246
Db 177359 CTGTGTTGCTTAACAAATTTTCACTTTCAAGTATTTTAAATATTTTAAAT 177300
QY 1247 TAACCAAGATGAGTTCTGATTTGATTTGAAAGCTTTCTTGGTTAAATAACAAGTA 1306
Db 177299 GAATTAATATGATGTTGCGGAGATTTTCAATCATTAATATTTGTGCAAGAAATG 177240
QY 1307 TATTACTAAACATTAAGAAAACATTTTGTGAAAAGAAATTAAGTTACTGACCC 1366
Db 177239 TATCTCTAATAATATTAATTCATTAATTTGAGAAAATTTGATTAATTTTCTAATGCT 177180
QY 1367 CATTTGACAGATGTCCTCATTAATATCTGATAGAAATAGAGCAATG 1414
Db 177179 ATTTGAAAAGATTACCGTTATTTGATATATNOCATTTTAAACATG 177132
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US-949-016-16915/c
/ Sequence 16915, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16915
/ LENGTH: 263694
/ TYPE: DNA
/ ORGANISM: Human
/ US-949-016-16915
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Query Match
Best Local Similarity 46.9%; Pred. No. 1.5; Length 263694;
Matches 135; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
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QY 1127 AACCATTAATAATTATTAATAATCTTCCACCATAGAAAAGTAATTTGATCAGCAT 1186
Db 177419 AAGCCATTAATAACCTTTCTAATCTCTAGATATTTGAAAACCTTTATGTTCTTCTGTC
QY 1187 GGAATTTTGTACAAAGTAGTATTTGATTTGAGAGTGTACTAGTAAGTATAC 1246
Db 177359 CTGTGTTGCTTAACAAATTTTCACTTTCAAGTATTTTAAATATTTTAAAT 177300
QY 1247 TAACCAAGATGAGTTCTGATTTGATTTGAAAGCTTTCTTGGTTAAATAACAAGTA 1306
Db 177299 GAATTAATATGATGTTGCGGAGATTTTCAATCATTAATATTTGTGCAAGAAATG 177240
QY 1307 TATTACTAAACATTAAGAAAACATTTTGTGAAAAGAAATTAAGTTACTGACCC 1366
Db 177239 TATCTCTAATAATATTAATTCATTAATTTGAGAAAATTTGATTAATTTTCTAATGCT 177180
QY 1367 CATTTGACAGATGTCCTCATTAATATCTGATAGAAATAGAGCAATG 1414
Db 177179 ATTTGAAAAGATTACCGTTATTTGATATATNOCATTTTAAACATG 177132
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## RESULT 8

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US-09-949-016-12968/c
/ Sequence 12968, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12968
/ LENGTH: 222452
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-12968
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Query Match
Best Local Similarity 49.3%; Pred. No. 2.2; Length 222452;
Matches 138; Conservative 0; Mismatches 141; Indels 1; Gaps 1;
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QY 1065 TCACACCCCAAGTAGGCTTACAGCTTTTCATTAATTAAGTAATCTTTTTCG 1124
Db 34351 TCTAAGATGAATGTGTGGAAGAAGTCAGTATTAATAATATTTTATTTAAT 34292
QY 1125 CTACCAATTAATAATTATTAATAATCTTCCACCATAGAAAAGTAAATTTGATCAGC 1184
Db 34291 ATTAAGAAAAGAAATATGATTAATAATTTCAAAATTTAGCTAATTAACACATTTGAAATCA 34232
QY 1185 ATGGAATTTTGTACAAAGTAGTATTTGATTTGGAGAGTCTAGTAAGTATAGT 1244
Db 34231 ATTTGTAATTTTATTTGACTTTTATTTTATTTGATTTGGAGAGAGAAC -AACCTTTATTTT 34173
QY 1245 ACTAACCAAGATGAGTTCTGATTTTGAATTTGAACTTTTCTTAAGTAAAAACAAG 1304
Db 34172 ATTAAGAAATTTCTTTCTTTTAAACACTGAAATTAAGCTTTTGAAGAAATGAAATATTTCT 34113
QY 1305 TATATTTACTAAACATTAAGAAAACATTTTGTGAAAAG 1344
Db 34112 GAAATTTCTAAGAAATGAACTGGAATAATGCTTTCAAG 34073
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RESULT 9  
US-08-076-090-1  
Sequence 1, Application US/08076090  
Patent No. 5631162  
GENERAL INFORMATION:  
APPLICANT: Leboulch, Philippe  
APPLICANT: London, Irving M.  
TITLE OF INVENTION: Retroviral Vectors for Transducing  
TITLE OF INVENTION: Beta-Globulin Gene and Beta-Locus Control Region  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kilpatrick & Cody  
STREET: 1100 Peachtree Street, Suite 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: U.S.  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/076, 090  
FILING DATE: 19930611  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: MIT 6128  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 815-6508  
TELEFAX: (404) 815-6555  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1666 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: Beta-globin gene  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 37..298  
OTHER INFORMATION: /note= "Exon III"  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 299..1148  
OTHER INFORMATION: /note= "Intron 2"  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 1149..1370  
OTHER INFORMATION: /note= "Exon II"  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 1371..1501  
OTHER INFORMATION: /note= "Intron 1"  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 1502..1643  
OTHER INFORMATION: /note= "Exon I"  
US-08-076-090-1  
Query Match 2.5%; Score 42.2; DB 1; Length 1666;  
Best Local Similarity 47.5%; Pred. No. 0.35;

Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;  
QY 1091 TTTTCCATTAATAATTAAGTAATCTTTTGGCCCAACCAATTAATAATTTATTTAAATC 1150  
DB 684 TGTGTACACATATTTAAACATTAACCAATTAATGATTAATGATTAATGATC 743  
QY 1151 TTTCACCATGAAAGTTAAATTTGATCAGCGATGAAATTTTGTCAAAAGTAGGT 1210  
DB 744 AATTGAAATTAAGAAATTAAGTAGGAGATTTGAAATGCAATTAAGCACATAT 803  
QY 1211 ATTTCAATTTGGAGTGTACTAGTAACCTAAGTAAGTAACTAAGTAAGTCTTGTATTT 1270  
DB 804 ATTCCAATTAAGTAAGTACTAGGACAGCTGTAAAGTTTATTAAGTTACTTATAT 863  
QY 1271 GGATTTGAGCTTTTCTTGTATTAATAACAGATATATTACTTAACATTAAGAAATA 1330  
DB 864 ATCTCAGATATTTTCCTTTGTATACCAATGTTAAGCATTAAGTAAGTAAGTAATA 923  
QY 1331 CATTTGTGAAAGAGAAATTA 1353  
DB 924 ATTCGGAGAGAGAAAGAAAG 946  
RESULT 10  
PCT-US94-06661-1  
Sequence 1, Application PC/TUS9406661  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Retroviral Vectors for Transducing  
TITLE OF INVENTION: Beta-Globulin Gene and Beta-Locus Control Region  
NUMBER OF SEQUENCES: 5  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06661  
FILING DATE: 10-JUN-1994  
CLASSIFICATION:  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1666 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
CELL TYPE: Beta-globin gene  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 37..298  
OTHER INFORMATION: /note= "Exon III"  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 299..1148  
OTHER INFORMATION: /note= "Intron 2"  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 1149..1370  
OTHER INFORMATION: /note= "Exon II"  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 1371..1501  
OTHER INFORMATION: /note= "Intron 1"  
FEATURE:  
NAME/KEY: misc\_signal  
LOCATION: 1502..1643  
OTHER INFORMATION: /note= "Exon I"

PCT-US94-06661-1

Query Match 2.5%; Score 42.2; DB 5; Length 1666;  
Best Local Similarity 47.5%; Pred. No. 0.35; Mismatches 138; Indels 0; Gaps 0;

Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

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QY 1091 TTTTCCATAAATTAAGTAATCTTTTGGCTAACCAATTAATAATTTGAAATC 1150
DB 684 TGTGACACATATTAAACATTACCTTAACCATTAATATATATATATATATATC 743
QY 1151 TTTCCAAACATAGAAAAGTTAAATTTGATCAGCATGGAATTTTGTACAAAGCTAGGT 1210
DB 744 AATTGAAATTAAGAAAATTAAGTAGGAGATTATGAATATGCAATATAGCACATAT 803
QY 1211 ATTTCATTGGAGTGTACTAGTAAGTAAGTAACTAACCAATGAGTTCTGATTTT 1270
DB 804 ATTCCAATATGATATGTAAGTACGACAGCTGTAAAGTTTTTTTAAGTTACTTAATGT 863
QY 1271 GGAATTTGAAGCTTTTCTTAGTTAAACAAAGTATTTACTTAACAAATTAAGAAAA 1330
DB 864 ATCTCAGAGATATTTCTTTTGTATACCAATGTTAAGCATTAAGTATTAAGTAAAA 923
QY 1331 CATTTTGTGAAAAGAGAAATAAA 1353
DB 924 ATTCGAGAGAGAAAAAAGAAAA 946
```

RESULT 11

US-08-550-715-10/C

Sequence 10, Application US/08550715

Patent No. 5750345

GENERAL INFORMATION:

APPLICANT: Bowie, Lemuel J.

TITLE OF INVENTION: Human  $\beta$ -Thalassemia Mutations as a Predictor of

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &amp; Borun

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/550,715

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gase, David A.

REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 28493/32834

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2500 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: CDS

LOCATION: join(687..778, 909..1131, 1982..2107)

US-08-550-715-10

Query Match 2.5%; Score 42.2; DB 1; Length 2500;

Best Local Similarity 47.5%; Pred. No. 0.41;  
Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

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RESULT 12

US-09-411-449-3/C

Sequence 3, Application US/09411449

Patent No. 6524851

GENERAL INFORMATION:

APPLICANT: James Ellis

TITLE OF INVENTION: HYBRID NUCLEIC ACID MOLECULES AND VECTORS INCLUDING

FILE REFERENCE: 11860017

CURRENT APPLICATION NUMBER: US/09/411,449

PRIOR FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: 2,246,005

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 3

LENGTH: 3385

TYPE: DNA

ORGANISM: Homo sapiens

US-09-411-449-3

Query Match 2.5%; Score 42.2; DB 4; Length 3385;  
Best Local Similarity 47.5%; Pred. No. 0.47;  
Matches 125; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

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RESULT 13

US-09-710-279-3535

Sequence 3535, Application US/09710279

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 07:18:54 ; Search time 1053.92 Seconds  
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Title: US-09-938-842a-3729

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Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1677	100.0	1677	US-09-938-842a-3729	Sequence 3729, Ap
3	50.6	3.0	8056	US-10-473-126-386	Sequence 386, App
4	49.6	3.0	8056	US-10-473-126-386	Sequence 7035, App
5	49.2	2.9	3673778	US-10-312-841-1	Sequence 2, Appli
6	49.2	2.9	3673778	US-10-312-841-1	Sequence 1, Appli
7	48.6	2.9	20933	US-10-433-793-154	Sequence 154, App
8	47.8	2.9	2958	US-09-938-842a-338	Sequence 338, App
9	47.8	2.9	2958	US-09-938-842a-338	Sequence 338, App
10	46.6	2.8	516	US-09-960-352-5785	Sequence 5785, Ap
11	46.6	2.8	789	US-10-282-122a-15640	Sequence 15640, A

12	46.4	2.8	610	US-10-021-333-8212	Sequence 8212, Ap
13	46.4	2.8	7047	US-10-240-453-259	Sequence 259, App
14	46.4	2.8	17848	US-10-239-676-28	Sequence 28, Appl
15	46.4	2.8	17848	US-10-240-453-38	Sequence 38, Appl
16	46.4	2.8	17848	US-10-257-166-58	Sequence 58, Appl
17	46.4	2.8	17848	US-10-473-166-58	Sequence 386, App
18	45.6	2.7	8056	US-10-433-793-28	Sequence 28, Appl
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22	45.2	2.7	502	US-09-814-353-17272	Sequence 2829, App
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24	44.8	2.7	1271	US-09-938-842a-2829	Sequence 4676, App
25	44.6	2.7	556	US-09-814-353-1676	Sequence 10975, A
26	44.6	2.7	556	US-09-814-353-10975	Sequence 4038, App
27	44.6	2.7	2000	US-09-938-842a-4038	Sequence 4038, App
28	44.6	2.7	2000	US-09-938-842a-4038	Sequence 6375, App
29	44.4	2.6	531	US-10-021-323-6375	Sequence 34, Appl
30	44.4	2.6	357652	US-10-322-636-34	Sequence 31704, A
31	44.2	2.6	449	US-10-424-599-31704	Sequence 1906, App
32	44.2	2.6	8711	US-10-311-455-1906	Sequence 218, App
33	44.2	2.6	19734	US-10-311-455-2148	Sequence 7430, App
34	44.2	2.6	113515	US-10-357-930-7430	Sequence 230, App
35	44.2	2.6	468	US-10-311-455-230	Sequence 4304, App
36	44	2.6	7498	US-10-424-599-4304	Sequence 112, App
37	43.8	2.6	12643	US-10-311-455-112	Sequence 257, App
38	43.6	2.6	11473	US-10-240-453-257	Sequence 254, App
39	43.6	2.6	11473	US-10-257-166-112	Sequence 386, App
40	43.4	2.6	6533	US-10-221-714A-254	Sequence 1, Appli
41	43.4	2.6	7008	US-10-221-714A-254	Sequence 138, App
42	43.4	2.6	15161	US-09-790-988-1	Sequence 9882, App
43	43.4	2.6	640681	US-10-621-901-138	
44	43.2	2.6	392	US-10-198-846-9862	
45	43.2	2.6	2338	US-10-198-846-9862	

#### ALIGNMENTS

RESULT 1  
US-09-938-842a-3729  
Sequence 3729, Application US/09938842A  
Patent No. US20020160378A1  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
TITLE OF INVENTION: SAME, AND METHODS OF USE  
FILE REFERENCE: SCRIPI300-3  
CURRENT APPLICATION NUMBER: US/09/938, 842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227, 866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264, 647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300, 111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 3729  
LENGTH: 1677  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842a-3729

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 3729, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Jun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SCRIPT300-3  
; CURRENT APPLICATION NUMBER: US/09/938, 842A  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227, 866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264, 647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300, 111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 3729  
; LENGTH: 1677  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-3729

Query Match 100.0%; Score 1677; DB 11; Length 1677;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1261 TTCTGATTTTGGATTTTGAAGCTTTTCTAGGTTTAAACCAAGTATTAATTAACAAT 1320
Db      1261 TTCTGATTTTGGATTTTGAAGCTTTTCTAGGTTTAAACCAAGTATTAATTAACAAT 1320
Qy      1321 AAAAGAAAAATTTTGTGAAAAGAAATTAAGTTTACTGGAACCCCATTTGACATGG 1380
Db      1321 AAAAGAAAAATTTTGTGAAAAGAAATTAAGTTTACTGGAACCCCATTTGACATGG 1380
Qy      1381 TCCCAATTAATTAATCTGATAGATAGAGCAATGGAAGTGTATTTGTCAGGTGACAA 1440
Db      1381 TCCCAATTAATTAATCTGATAGATAGAGCAATGGAAGTGTATTTGTCAGGTGACAA 1440
Qy      1441 TCGGAATGGTCTTTTAAAGCTCATCGAACACATCAGAACCGTTGATTTTCCCGCATCAA 1500
Db      1441 TCGGAATGGTCTTTTAAAGCTCATCGAACACATCAGAACCGTTGATTTTCCCGCATCAA 1500
Qy      1501 AAAGCTTGAATATCTATCTCACTTGTCTTCTGCTCTATATATATATCTGACGAGTC 1560
Db      1501 AAAGCTTGAATATCTATCTCACTTGTCTTCTGCTCTATATATATATCTGACGAGTC 1560
Qy      1561 AATTTAGTAAATCTCTTGGAGTGAACGGCTTAAACGATTTCTTCCATTTGATCC 1620
Db      1561 AATTTAGTAAATCTCTTGGAGTGAACGGCTTAAACGATTTCTTCCATTTGATCC 1620
Qy      1621 GCTTTTAAACAATCTGTCGTATCTCCACCGTCTTCTGAGCTATATTTTA 1677
Db      1621 GCTTTTAAACAATCTGTCGTATCTCCACCGTCTTCTGAGCTATATTTTA 1677

RESULT 3
US-10-473-126-386
; Sequence 386, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match      3 0%; Score 50.6; DB 18; Length 8056;
Best Local Similarity 49.4%; Pred. No. 0.63;
Matches 131; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

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US-10-312-841-1

Query Match	2.9%	Score 47.8	DB 11	Length 2958
Best Local Similarity	50.7%	Pred. No. 1.8		
Matches 115, Conservative	0	Mismatches 112	Indels 0	Gaps 0

Db 410 ATTACCACTGCTAGTATTAAGTCTTTTGTGTTACCAAGTATTTTACAGGGTTCATC 351  
Qy 1288 TTAGGTTAAAAACAAGTATTTACTTAACAATTAAGAAAAACATTTTGTGAAGAG 1347  
Db 350 ATTAATTAAGAGAGATTAATTTACTTAATATGCAAAAAACAACGTTAAATATAGCA 291  
Qy 1348 AATAAGTTTACTGAGACCCCATTTGACAGATGCTCCATTAATTAATCTGATAGAGATG 1407  
Db 290 GAGAAAGGTTTGTGCAATTGTGCAATGCACTGACATTTATCAAGAGTGAATATGAC 231  
Qy 1408 AGCATGGAAGTATTTGTTACGTTGTAATTCGATGTTCTT 1454  
Db 230 AAAACAATCCTTGTTGTTGCAAGTTCAACAGTAGGCGAGACACTT 184

RESULT 10  
US-09-960-352-5785/c  
Sequence 5785, Application US/09960352  
Patent No. US20020137139A1  
GENERAL INFORMATION:  
APPLICANT: Warren, Wesley C.  
APPLICANT: Tao, Nengbing  
APPLICANT: Byatt, John C.  
APPLICANT: Mathialagan, Nagappan  
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
FILE REFERENCE: 16511.006/37-21 (10298)C  
CURRENT APPLICATION NUMBER: US/09/960,352  
CURRENT FILING DATE: 2001-09-24  
NUMBER OF SEQ ID NOS: 15112  
SEQ ID NO 5785  
LENGTH: 516  
TYPE: DNA  
ORGANISM: Bos taurus  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (76), (90)  
OTHER INFORMATION: unsure at all n locations  
US-09-960-352-5785  
OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1

Query Match  
Best Local Similarity 2.8%; Score 46.6; DB 9; Length 516;  
Matches 154; Conservative 0; Mismatches 179; Indels 0; Gaps 0;  
Qy 1098 ATAAATTAAGTAAATCTTTTGGCTTACCAATTAATTAATTAATCTTTCCAA 1157  
434 ATAAATTAAGTAAATCTTTTGGCTTACCAATTAATTAATTAATCTTTCCAA 1157  
Qy 1158 CCATGAGAAAGTAAATTTGATCGCATGAAATTTTGTACAAAGCTAGTATTCAT 1217  
374 TAAATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 315  
Db 1218 TTGGAGTGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGT 1277  
314 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 255  
Qy 1278 GAAAGCTTTCTTGTGTTAAAAACAAGTATTAATTAATTAATTAATTAATTAATTAATTA 1337  
254 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 195  
Db 1338 TGAAGAGAGAAATTAAGTTTACGAGCCCATTTGACAGATGCTCCATTAATTAATTAATTA 1397  
194 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 135  
Qy 1398 TAGAGATGAGCAATGAGAAAGTATTTGTGCA 1430  
Db 134 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 102

RESULT 11  
US-10-282-122A-15640

Sequence 15640, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zykkind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15640  
LENGTH: 789  
TYPE: DNA  
ORGANISM: Clostridium acetobutylicum  
US-10-282-122A-15640

Query Match  
Best Local Similarity 2.8%; Score 46.6; DB 17; Length 789;  
Matches 133; Conservative 0; Mismatches 144; Indels 0; Gaps 0;  
Qy 1074 AAGTATGGGCTTACAGCTTTTCCATTAATTAAGTAAATCTTTTGGCTTACCAAT 1133  
52 AAAAAAGCGCTTACCTTAAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 111  
Db 1134 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1193  
112 AGAAATTTTAAGAACTCTCGAAAAAGAAATTAATTAATTAATTAATTAATTAATTAATTA 171  
Qy 1194 TTTGTACAAAGCTAGTATTTGATTTGGAGTGTACTAGTACTAGTACTAGTACTAGTACTAG 1253  
172 GCATCCACATCTTAAGGAGTTTAAGGAAAGTTTAATCCCGTAAATTAAGCAAAATT 231  
Db 1254 AATGAGTTTCTGATTTTGGATTTTGAACCTTTTCTTGAAGTTTAAACCAAGTAAATTAATTA 1313  
232 TATGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 291  
Qy 1314 AAACATTAAGAAACAAATTTTGTGAAGAGAAAT 1350  
Db 292 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 328

RESULT 12  
US-10-021-323-8212  
Sequence 8212, Application US/10021323  
Publication No. US20040123340A1  
GENERAL INFORMATION:  
APPLICANT: Deikman, Jill  
APPLICANT: Feng, Paul C.C.  
APPLICANT: Fincher, Karen L.  
APPLICANT: Ziegler, Todd E.  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(52274)B  
CURRENT APPLICATION NUMBER: US/10/021,323  
CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: US 60/255, 619  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 17880  
SEQ ID NO 8212  
LENGTH: 610  
TYPE: DNA  
ORGANISM: *Gossypium hirsutum*  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB828-007-Q1-K6-G2  
US-10-021-323-8212  
Query Match  
Best Local Similarity 2.8%; Score 46.4; DB 18; Length 610;  
Matches 98; Conservative 0; Mismatches 86; Indels 0; Gaps 0;  
QY 1169 TTAATTTATGATGAGATGAAATTTTGTACAAAGCTAGTATTCATTGGAGAGTGA 1228  
DB 152 TTGAGTTCAATGCTATGATGAAATTTTGTCCAAAGTTGATTTTAATTTCTCATGTT 211  
QY 1229 CTAGTACTAGTACTGATCAACAGATGATGTTTGTGATTTGGATTTGAAGCTTTTCT 1288  
DB 212 ATTAACAACTATGATGAAATTCACATTTATGTTATGTTCTAGTGTATTTATCTTAT 271  
QY 1289 TAGGTTAAAAACAATATATTTACTAAACAATTAAGAAAAACATTTTGGAAAAAGAA 1348  
DB 272 TAAAAAATAA 331  
QY 1349 ATAA 1352  
DB 332 AAAA 335  
RESULT 13  
US-10-240-453-259  
Sequence 259, Application US/10240453  
Publication No. US20030148326A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENBROCK, Christian  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA  
TITLE OF INVENTION: Transcription  
TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated  
FILE REFERENCE: 5013.1009  
CURRENT APPLICATION NUMBER: US/10/240,453  
CURRENT FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: PCT/EP01/03973  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: DE 10019058.8  
PRIOR FILING DATE: 2000-04-06  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: DE 10032529.7  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 350  
SEQ ID NO 259

LENGTH: 7047  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (*Homo sapiens*)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (182)  
US-10-240-453-259  
Query Match  
Best Local Similarity 2.8%; Score 46.4; DB 15; Length 7047;  
Matches 145; Conservative 0; Mismatches 146; Indels 1; Gaps 1;  
QY 1084 TTACAGCTTTTCCATTAATTAAGTAATCTTTTGGCTTACCATTAATTAATAT 1143  
DB 3514 TTATATATGATATATGATTAAGTTTATGAAATTTATTTTATTTATTTAGAGAAAT 3573  
QY 1144 GAAATCTTCCACATGAAAGTAATTAATTTGATCAGCATGAAATTTTGTACAA 1203  
DB 3574 GAAATTTCCGTTATATTA-AAAATTTGATACGAATGTTTATAGATTTTATTTGTAA 3632  
QY 1204 GCTAGTATTTCAATTTGGAGTGTACTAGTAACATGATACAAAGATGAGTTTC 1263  
DB 3633 TGGTGAATTTGTAGTATTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTT 3692  
QY 1264 TGATTTGATTTTGAAGCTTTTCTTATGTTTAAAAACAGATATTAATTAACATTA 1323  
DB 3693 TTAATGATTAATTAAGAAATTTGTTATTTGTAATTAATTAATTTATTTATTTATA 3752  
QY 1324 AGAAAAATTTTGTGAAAGAAATTAATTAATTTTCTGAGCCCATTTGTACA 1375  
DB 3753 ATTAATTAATTAATTTTAAGGAATTAATTTGATGAGTAAATTAATTAATTA 3804  
RESULT 14  
US-10-239-676-28/c  
Sequence 28, Application US/10239676  
Publication No. US20030082609A1  
GENERAL INFORMATION:  
APPLICANT: OLEK, Alexander  
APPLICANT: PIEPENBROCK, Christian  
APPLICANT: BERLIN, Kurt  
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation  
FILE REFERENCE: 5013.1003  
CURRENT APPLICATION NUMBER: US/10/239,676  
CURRENT FILING DATE: 2002-09-24  
PRIOR APPLICATION NUMBER: PCT/EP01/03968  
PRIOR FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: DE 10019058.8  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: DE 10019173.8  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: DE 10043826.1  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 228  
SEQ ID NO 28  
LENGTH: 17848  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (*Homo sapiens*)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (6075, 8510, 8516, 8680, 9019, 15666)  
US-10-239-676-28  
Query Match  
Best Local Similarity 2.8%; Score 46.4; DB 14; Length 17848;  
Matches 164; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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QY 1088 AGCTTTTCATTAATAAGTAATCTTTTGGCTAACATTAATAATTATTTGAAA 1147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10047 AACTTAATAAATAACATTTTAAAAATTTAAAAATTAACCTTAATTAATTAATTCAA 9988
QY 1148 ATCTTCCACCAATGAAAGTTAAATTTGATCAGCATGAAATTTTGACAAAGCTA 1207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9987 AAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATC 9928
QY 1208 GGTATTTCTAGTGGAGTGTCTAGTACTAGTACTAGTACTAGTACTAGTACTAGT 1267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9927 ATAAATAATATACCTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATTCCTTT 9868
QY 1268 TTGGATTTTGAAGCTTTTCTAGTAAATAAATAAATAAATAAATAAATAAATAAATAAAGAA 1327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9867 TATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 9808
QY 1328 AAACATTTTGGAAAGAAATTAAGTTTACTGACCCCATTTGACAGATGCTCCATA 1387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9807 AATTAAATTAATCGAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 9748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1388 ATAAATCTGATGAGATGAGCATGCAATGCAATGCTTGTTCACGTGATCAATGGAAAT 1447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9747 AAATCTATTACCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATC 9688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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## RESULT 15

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US-10-240-453-38/C
; Sequence 38, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: By Means of Assessing the Methylation Status of Genes Associated
; FILE REFERENCE: 5013.1009
; CURRENT APPLICATION NUMBER: US/10/240,453
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03973
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 38
; LENGTH: 17848
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (6075, 8510, 8516, 8680, 9019, 15666)
US-10-240-453-38
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Query Match 2.8%; Score 46.4; DB 15; Length 17848;  
Best Local Similarity 45.6%; Pred. No. 8.7;

Matches 164; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

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QY 1088 AGCTTTTCATTAATAAGTAATCTTTTGGCTAACATTAATAATTATTTGAAA 1147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 10047 AACTTAATAAATAACATTTTAAAAATTTAAAAATTAACCTTAATTAATTAATTCAA 9988
QY 1148 ATCTTCCACCAATGAAAGTTAAATTTGATCAGCATGAAATTTTGACAAAGCTA 1207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9987 AAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATC 9928
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 1208 GGTATTTCTAGTGGAGTGTCTAGTACTAGTACTAGTACTAGTACTAGTACTAGT 1267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9927 ATAAATAATATACCTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATTCCTTT 9868
QY 1268 TTGGATTTTGAAGCTTTTCTAGTAAATAAATAAATAAATAAATAAATAAATAAATAAAGAA 1327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9867 TATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 9808
QY 1328 AAACATTTTGGAAAGAAATTAAGTTTACTGACCCCATTTGACAGATGCTCCATA 1387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9807 AATTAAATTAATCGAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 9748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1388 ATAAATCTGATGAGATGAGCATGCAATGCAATGCTTGTTCACGTGATCAATGGAAAT 1447
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9747 AAATCTATTACCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATC 9688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 12:00:51 ; Search time 210.848 Seconds  
(without alignments)  
8311.439 Million cell updates/sec

Title: US-09-938-842A-1034

Perfect score: 1071  
Sequence: 1 atggcgacatcgaagct.....cagcgatcgcgaaccactga 1071

Scoring table: OLIGO-NUC  
Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

W size: 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/PTCUTS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match Length	ID	Description
1	1.9	78810	US-09-949-016-16198	Sequence 16198, A
2	1.8	2556	US-09-489-039A-6112	Sequence 6112, Ap
3	1.8	34094	US-09-292-034-1	Sequence 1, Appl
4	1.8	168394	US-09-949-016-13002	Sequence 13002, A
5	1.8	372	US-09-902-540-5948	Sequence 5948, Ap
6	1.7	1527	US-09-489-039A-716	Sequence 716, App
7	1.7	1720	US-09-902-540-198	Sequence 198, App
8	1.7	4261	US-09-976-594-3	Sequence 16873, A
9	1.7	35688	US-09-949-016-16873	Sequence 12101, A
10	1.7	94879	US-09-949-016-12101	Sequence 13393, A
11	1.7	94884	US-09-949-016-13393	Sequence 1, Appl
12	1.7	162450	US-09-345-882-1	Sequence 14033, A
13	1.7	784019	US-09-949-016-14033	Sequence 12777, A
14	1.7	828152	US-09-949-016-12777	Sequence 1, Appl
15	1.7	1664976	US-08-916-421B-1	Sequence 24082, A
16	1.7	1664976	US-09-692-570-1	Sequence 1834, Ap
17	1.6	318	US-09-513-999C-24082	Sequence 12761, A
18	1.6	338	US-09-640-211A-1834	Sequence 186, App
19	1.6	396	US-09-248-796A-12761	Sequence 454, A
20	1.6	447	US-09-328-352-186	Sequence 15736, A
21	1.6	494	US-09-270-767-454	Sequence 2, Appl
22	1.6	494	US-08-510-878-2	Sequence 178644, Sequence 178645, Sequence 178646, Sequence 184362,
23	1.6	516	US-09-510-878-2	
24	1.6	601	US-09-949-016-178644	
25	1.6	601	US-09-949-016-178645	
26	1.6	601	US-09-949-016-178646	
27	1.6	601	US-09-949-016-184362	

28	1.6	601	US-09-949-016-184363	Sequence 184363, Sequence 459, App
29	1.6	675	US-09-640-211A-459	Sequence 3, Appl
30	1.6	748	US-08-510-878-3	Sequence 13769, A
31	1.6	779	US-09-270-767-13769	Sequence 1054, App
32	1.6	864	US-09-976-594-1054	Sequence 385, App
33	1.6	864	US-09-919-039-385	Sequence 6878, Ap
34	1.6	867	US-09-252-991A-6878	Sequence 6792, Ap
35	1.6	882	US-09-252-991A-6792	Sequence 59, Appl
36	1.6	900	US-09-050-739-59	Sequence 81, Appl
37	1.6	1251	US-09-614-912-81	Sequence 9103, Ap
38	1.6	1290	US-09-902-540-9103	Sequence 1, Appl
39	1.6	1353	US-08-611-280-1	Sequence 1, Appl
40	1.6	1353	US-09-195-940-1	Sequence 69, Appl
41	1.6	1353	US-09-562-466-1	Sequence 3108, Ap
42	1.6	1636	US-09-614-912-69	Sequence 42, Appl
43	1.6	1758	US-09-489-039A-3108	Sequence 1, Appl
44	1.6	1960	US-09-553-867A-42	
45	1.6	3758	US-08-323-477-1	

#### ALIGNMENTS

```
RESULT 1
US-09-949-016-16198
Sequence 16198, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16198
LENGTH: 78810
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(78810)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16198

Query Match 1.9%; Score 20; DB 4; Length 78810;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1029 CCACTTCATGACACACCA 1048
DB 17829 CCACTTCATGACACCA 17848

RESULT 2
US-09-489-039A-6112
Sequence 6112, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
```

;; PRIOR FILING DATE: 1999-01-29  
;; NUMBER OF SEQ ID NOS: 14342  
;; SEQ ID NO 6112  
;; LENGTH: 2556  
;; TYPE: DNA  
;; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-6112

Query Match  
Best Local Similarity 1.8%; Score 19; DB 4; Length 2556;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 AGCTCAGCGCTTCGACA 198  
DB 850 AGCTCAGCGCTTCGACA 868

## RESULT 3

US-09-292-034-1  
Sequence 1, Application US/09292034  
Patent No. 6492343  
GENERAL INFORMATION:

APPLICANT: Reddy, P. Seshidhar  
APPLICANT: Tikoo, Suresh  
APPLICANT: Babituk, Lorne  
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME  
FILE REFERENCE: 293102002400  
CURRENT APPLICATION NUMBER: US/09/292,034  
CURRENT FILING DATE: 1999-04-14  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 34094  
TYPE: DNA  
ORGANISM: Porcine Adenovirus Type 3  
FEATURE:

Query Match  
Best Local Similarity 1.8%; Score 19; DB 4; Length 34094;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 850 AGCAGCGGCTTGTATCGG 868  
DB 21527 AGCAGCGGCTTGTATCGG 21545

## RESULT 4

US-09-949-016-13002/C  
Sequence 13002, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13002

LENGTH: 168394  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(168394)

;; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13002

Query Match  
Best Local Similarity 1.8%; Score 19; DB 4; Length 168394;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 TTTCAGCTTCTCGGTTT 563  
DB 77366 TTTCAGCTTCTCGGTTT 77348

## RESULT 5

US-09-902-540-5948  
Sequence 5948, Application US/09902540  
Patent No. 6833447  
GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Wiegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 5948  
LENGTH: 372  
TYPE: DNA  
ORGANISM: Myxococcus xanthus  
US-09-902-540-5948

Query Match  
Best Local Similarity 1.7%; Score 18; DB 4; Length 372;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 GCCCGTATGCGCGTGT 167  
DB 234 GCCCGTATGCGCGTGT 251

## RESULT 6

US-09-489-039A-716  
Sequence 716, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 716  
LENGTH: 1527  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-716

Query Match  
Best Local Similarity 1.7%; Score 18; DB 4; Length 1527;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 AGCGGAGCGGTATGC 160  
DB 965 AGCGGAGCGGTATGC 982

## RESULT 7

US-09-902-540-198  
; Sequence 198, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(13849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 198  
; LENGTH: 1720  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; US-09-902-540-198

Query Match 1.7%; Score 18; DB 4; Length 1720;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 GCCGGTATGCCGCTT 167  
Db 234 GCCGGTATGCCGCTT 251

RESULT 8  
US-09-976-594-3/C  
; Sequence 3, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; APPLICANT: Buchbinder, Jenny  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LAYER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-004 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 3  
; LENGTH: 4261  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. 6673549 1863336CBI  
; US-09-976-594-3

Query Match 1.7%; Score 18; DB 4; Length 4261;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 603 AGCTCTGGCATCATCCAC 620  
Db 3322 AGCTCTGGCATCATCCAC 3305

RESULT 9  
US-09-949-016-16873/C  
; Sequence 16873, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16873  
; LENGTH: 35688  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-16873

Query Match 1.7%; Score 18; DB 4; Length 35688;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 473 TGGGTGAATCTGATGA 490  
Db 30454 TGGGTGAATCTGATGA 30437

RESULT 10  
US-09-949-016-12101/C  
; Sequence 12101, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12101  
; LENGTH: 94879  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1) -(94879)  
; OTHER INFORMATION: n = A,T,C or G  
; US-09-949-016-12101

Query Match 1.7%; Score 18; DB 4; Length 94879;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 510 TTCTAAGTGTGATATAT 527  
Db 76650 TTCTAAGTGTGATATAT 76633

RESULT 11  
US-09-949-016-13393/C  
; Sequence 13393, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: PastSeq for Windows Version 4.0  
SEQ ID NO: 13393  
LENGTH: 94884  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1) - (94884)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13393

Query Match 1.7%; Score 18; DB 4; Length 94884;  
St Local Similarity 100.0%; Pred. No. 46;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 510 TTCTACGCGTGGTAT 527  
DB 76650 TTCTACGCGTGGTAT 76633

RESULT 12  
US-09-345-882-1  
Sequence 1, Application US/09345882  
Patent No. 6399373  
GENERAL INFORMATION:  
APPLICANT: Bougenetec, Lydie  
TITLE OR INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)  
FILE REFERENCE: GENSET 031A  
CURRENT APPLICATION NUMBER: US/09/345,882  
PRIOR FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: US 60/091,315  
PRIOR FILING DATE: 1998-06-30  
PRIOR APPLICATION NUMBER: US 60/111,909  
PRIOR FILING DATE: 1998-12-10  
NUMBER OF SEQ ID NOS: 140  
SOFTWARE: Patent.pm  
SEQ ID NO 1  
LENGTH: 162450  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 72794  
OTHER INFORMATION: 5-124-273 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 88073  
OTHER INFORMATION: 5-127-261 : polymorphic base A or C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 90842  
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 93714  
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT  
FEATURE:  
NAME/KEY: allele  
LOCATION: 97122  
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 97152  
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T  
FEATURE:

NAME/KEY: allele  
LOCATION: 99098  
OTHER INFORMATION: 5-130-257 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 99117  
OTHER INFORMATION: 5-130-276 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 103806  
OTHER INFORMATION: 5-131-395 : polymorphic base A or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 106940  
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A  
FEATURE:  
NAME/KEY: allele  
LOCATION: 108106  
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A  
FEATURE:  
NAME/KEY: allele  
LOCATION: 108149  
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT  
FEATURE:  
NAME/KEY: allele  
LOCATION: 108308  
OTHER INFORMATION: 5-135-357 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 108471  
OTHER INFORMATION: 5-136-174 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 134134  
OTHER INFORMATION: 5-140-120 : polymorphic base C or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 134362  
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A  
FEATURE:  
NAME/KEY: allele  
LOCATION: 134374  
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA  
FEATURE:  
NAME/KEY: allele  
LOCATION: 146328  
OTHER INFORMATION: 5-143-84 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 146345  
OTHER INFORMATION: 5-143-101 : polymorphic base A or C  
FEATURE:  
NAME/KEY: allele  
LOCATION: 150329  
OTHER INFORMATION: 5-145-24 : polymorphic base A or G  
FEATURE:  
NAME/KEY: allele  
LOCATION: 160031  
OTHER INFORMATION: 5-148-352 : polymorphic base G or T  
FEATURE:  
NAME/KEY: allele  
LOCATION: 72771..72817  
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30  
FEATURE:  
NAME/KEY: allele  
LOCATION: 72771..72817  
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID31  
FEATURE:  
NAME/KEY: allele  
LOCATION: 88050..88096  
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31  
FEATURE:  
NAME/KEY: allele

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LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130

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OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
Query Match
Best Local Similarity 1.7%; Score 18; DB 3; Length 162450;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 35413 TCGAGACTTCTCTTGA 712
Qy 695 TCGAGACTTCTCTTGA 712
|||||
Db 35413 TCGAGACTTCTCTTGA 35430
Qy 695 CTGAGAGCTTCTCCCTA 1002
|||||
Db 136173 CTGAGAGCTTCTCCCTA 136156
|||||
RESULT 14
US-09-949-016-12777/C
Sequence 12777, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
Query Match
Best Local Similarity 1.7%; Score 18; DB 4; Length 784019;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 136173 CTGAGAGCTTCTCCCTA 136156
Qy 985 CTGAGAGCTTCTCCCTA 1002
|||||
Db 136173 CTGAGAGCTTCTCCCTA 136156
|||||
RESULT 14
US-09-949-016-12777/C
Sequence 12777, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

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;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 12777
;; LENGTH: 828152
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;;   NAME/KEY: misc_feature
;;   LOCATION: (1)...(828152)
;;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12777

Query Match      1.7%; Score 18; DB 4; Length 828152;
Best Local Similarity 100.0%; Pred.No. 44;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      985 CTGAGAGACTCTCCCTA 1002
      132306 CTGAGAGACTCTCCCTA 132289

RESULT 15
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
; Patent No. 6503729
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84808)..(84808)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
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;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc_feature
;; LOCATION: (103998)..(103998)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc_feature
;; LOCATION: (148948)..(148948)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc_feature
;; LOCATION: (163385)..(163385)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc_feature
;; LOCATION: (191995)..(191995)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc_feature
;; LOCATION: (231980)..(231980)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc_feature
;; LOCATION: (234187)..(234187)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc_feature
;; LOCATION: (234220)..(234220)
;; OTHER INFORMATION: n equals a, t, c, or g
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Best Local Similarity 100.0%, Pred. No. 43;
Matches 18, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 60.0, Gapext 60.0

Searched: 5394803 seqs, 2962729879 residues

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Minimum DB seq length: 0  
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Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1071	100.0	1071	11	US-09-938-842A-1034
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4	286	26.7	453	9	US-09-770-444-615
5	185	17.3	185	9	US-09-770-696-257
6	25	2.3	704	17	US-10-225-066A-1049
7	25	2.3	704	17	US-10-374-780A-2689
8	23	2.1	390	11	US-09-732-627A-4287
9	23	2.1	587	18	US-10-021-323-15482
10	23	2.1	938	18	US-10-767-795-3984
11	23	2.1	1604	15	US-10-295-403-147

12	23	2.1	1604	17	US-10-412-699B-551	Sequence 551, App
13	21	2.0	755	18	US-10-363-345A-33693	Sequence 33693, A
14	21	2.0	755	18	US-10-363-345A-33694	Sequence 33694, A
15	20	1.9	432	18	US-10-425-115-164143	Sequence 164143, A
16	20	1.9	442	17	US-10-424-599-59834	Sequence 59834, A
17	20	1.9	453	17	US-10-276-774-292	Sequence 292, App
18	20	1.9	1263	17	US-10-369-493-17704	Sequence 37704, A
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43	18	1.7	277	9	US-09-294-093B-4716	Sequence 4716, App
44	18	1.7	317	18	US-10-767-701-18118	Sequence 18118, A
45	18	1.7	364	10	US-09-918-995-30316	Sequence 30316, A

#### ALIGNMENTS

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Sequence 1034, Application US/09938842A  
Patent No. US20020160378A1  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
FILE REFERENCE: SCRIPT300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 1034  
LENGTH: 1071  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-1034

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1071; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db	121	CCCAACAGTAGTCTCGAGCCCAAGGCGGAGCGCGGTGATGCCGTGTTTTCAATGTCTTTA	180
QY	181	GCTCCACCGTCTTGCACAGGACCAACATTTGAGAGACCTTCGACTTAAAGACCGTCAACG	240
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3  ; GENERAL INFORMATION:
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5  ; APPLICANT: Harper, Jeff
6  ; APPLICANT: Kreps, Joel
7  ; APPLICANT: Wang, Xun
8  ; APPLICANT: Zhu, Tong
9  ;
10 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
11 ; TITLE OF INVENTION: SAME, AND METHODS OF USE
12 ;
13 ; FILE REFERENCE: SCRIPT300-3
14 ;
15 ; CURRENT APPLICATION NUMBER: US/09/938,842A
16 ;
17 ; PENDING FILING DATE: 2001-08-24
18 ;
19 ; PRIOR APPLICATION NUMBER: US 60/227,866
20 ;
21 ; PRIOR FILING DATE: 2000-08-24
22 ;
23 ; PRIOR APPLICATION NUMBER: US 60/264,647
24 ;
25 ; PRIOR FILING DATE: 2001-01-16
26 ;
27 ; PRIOR APPLICATION NUMBER: US 60/300,111
28 ;
29 ; PRIOR FILING DATE: 2001-06-22
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31 ; NUMBER OF SEQ ID NOS: 5379
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33 ; SEQ ID NO 1034
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35 ; LENGTH: 1071
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37 ; TYPE: DNA
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39 ; ORGANISM: Arabidopsis thaliana
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41 ; US-09-938-842A-1034

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Qy 841 GTTGTTCACAGAGCGGCTTGTATCCGTTTCAGAGTTAGCGGTTGCAATTTACAA 900
Db 841 GTTGTTCACAGAGCGGCTTGTATCCGTTTCAGAGTTAGCGGTTGCAATTTACAA 900
Qy 901 GCGAGCTGCTTATGAGTCCAGCTCAAGCTCAGGCTGATCAACCGGTATGCTGCA 960
Db 901 GCGAGCTGCTTATGAGTCCAGCTCAAGCTCAGGCTGATCAACCGGTATGCTGCA 960
Qy 961 ATTGCAACAACAAGCAGCAGCGTGAAGACTTCTCCCTAGATATTAAGAAACAA 1020
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Qy 1021 GAGCTTCAACAGTTATGAGCACAACAAGCAGGCTATCGAACCACTGA 1071
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## RESULT 3

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US-09-924-035A-502/c
; Sequence 502, Application US/09924035A
; Patent No. US20020142319A1
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; APPLICANT: Grlach, Jrm
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924,035A
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,784
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; SOFTWARE: FastSeq for Windows Version 3.0
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Best Local Similarity 99.6%; Pred. No. 1.5e-148;

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Qy 1020 AGAGCTTCAACAGTTATGAGCACAACAAGCAGGCTAT 1060
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## RESULT 4

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US-09-770-444-615/c
; Sequence 615, Application US/09770444
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; Patent No. US2002023280A1
; GENERAL INFORMATION:
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; APPLICANT: Goriach, Jorm
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moesner, Jeffrey P.
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Hoffman, Neil
; APPLICANT: Hutban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 615
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; ORGANISM: Arabidopsis thaliana
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n = A,T,C or G
US-09-770-444-615
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Best Local Similarity 100.0%; Pred. No. 6.8e-147;

Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 835 TTACAAGTTGTTCAAGAGAGGCTTGTATCCGTTTACAGCGTTAGGGTTCAATTA 894
Db 226 TTACAAGTTGTTCAAGAGAGGCTTGTATCCGTTTACAGCGTTAGGGTTCAATTA 167
Qy 895 TCAAGAGCAGTGTGTTATGCTCCAGCTCAAGCTCAGGCTTAACAACCGGTAGTTCA 954
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Db 166 TCAGAGGACGTCGATATGCTCCGAGCTCAAGCTCAGCGCTAACACCGGTAGTTCA 107  
Qy 955 TCGTCATTTGCAACAACAAGACGACACGCTGAGAGACTTCTCCCTAGAGATATACGAG 1014  
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RESULT 5  
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; Sequence 257, Application US/09770696  
; Patent No. US2001004940A1  
; GENERAL INFORMATION:  
; APPLICANT: Gorlach, Jörn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Moesener, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krieker, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hubban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2031US (PAPA-020PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,696  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,278  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 911  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 257  
; LENGTH: 185  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; 9-770-696-257

Query Match 17.3%; Score 185; DB 9; Length 185;  
Best Local Similarity 100.0%; Pred. No. 4.3e-91;  
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 35 GCAAGATCAACCTTAAGCCGCTGATTAACCTCAATCAACGGCGTCAGAAACGTG 94  
Db 1 GCAAGATCAACCTTAAGCCGCTGATTAACCTCAATCAACGGCGTCAGAAACGTG 60  
Qy 95 AAACCTCAAGACCTTTCCAAATCCCAAGTCAAGTCCAGAGCCCAAGGGGAGCCGG 154  
Db 61 AAACCTCAAGACCTTTCCAAATCCCAAGTCAAGTCCAGAGCCCAAGGGGAGCCGG 120  
Qy 155 TGATGCCGTCGTTTCAATCTCTTAACTGCTCAACCGCTTTCAGACAGACCATTTGAGA 214  
Db 121 TGATGCCGTCGTTTCAATCTCTTAACTGCTCAACCGCTTTCAGACAGACCATTTGAGA 180  
Qy 215 GAGCT 219  
Db 181 GAGCT 185

RESULT 6

US-10-225-066A-1049  
; Sequence 1049, Application US/10225066A  
; Publication No. US20030226173A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Adam, Luc J  
; APPLICANT: DUBEL, Arnold T  
; APPLICANT: HEARD, Jacqueline E  
; APPLICANT: PILGRIM, Marsha L  
; APPLICANT: JIANG, Cai-Zhong  
; APPLICANT: REUBER, T. Lynne  
; APPLICANT: CREELMAN, Robert A  
; APPLICANT: PINEDA, Omaira  
; APPLICANT: YU, Guo-Liang  
; APPLICANT: BROUN, Pierre E  
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants  
; FILE REFERENCE: MB10036-2 US  
; CURRENT APPLICATION NUMBER: US/10/225,066A  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 09/837,444  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: 60/310,847  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/336,049  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,692  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: 10/171,468  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 1122  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1049  
; LENGTH: 704  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; US-10-225-066A-1049

Query Match 2.3%; Score 25; DB 17; Length 704;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 222 GACTTAAGACCGTCACACGAAAGTT 246  
Db 189 GACTTAAGACCGTCACACGAAAGTT 213

RESULT 7  
US-10-374-780A-2689  
; Sequence 2689, Application US/10374780A  
; Publication No. US20040019927A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, Bradley K  
; APPLICANT: Riechmann, Jose Luis  
; APPLICANT: Jiang, Cai-Zhong  
; APPLICANT: Heard, Jacqueline E  
; APPLICANT: Haake, Volker  
; APPLICANT: Creelman, Robert A  
; APPLICANT: Ratcliffe, Oliver  
; APPLICANT: Adam, Luc J  
; APPLICANT: Reuber, T. Lynne  
; APPLICANT: Keddle, James  
; APPLICANT: Broun, Pierre E  
; APPLICANT: Pilgrim, Marsha L  
; APPLICANT: DUBEL III, Arnold T  
; APPLICANT: PINEDA, Omaira  
; APPLICANT: YU, Guo-Liang  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
; FILE REFERENCE: MB1-0047 CIP  
; CURRENT APPLICATION NUMBER: US/10/374,780A  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: 09/837,944

PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/934,455  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
PRIOR APPLICATION NUMBER: 10/225,066  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,067  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,068  
PRIOR FILING DATE: 2002-08-09  
NUMBER OF SEQ ID NOS: 2906  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO: 2689  
LENGTH: 704  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
OTHER INFORMATION: G1663  
US-10-374-780A-2689

Query Match 2.3%; Score 25; DB 17; Length 704;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GACTAAGACCGTCACGAGAGTT 246  
DB 189 GACTAAGACCGTCACGAGAGTT 213

RESULT 8  
US-09-732-627A-4287  
Sequence 4287, Application US/09732627A  
Publication No. US2004012338A1  
GENERAL INFORMATION:  
APPLICANT: Fincher, Karen L.  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(51770)B  
CURRENT APPLICATION NUMBER: US/09/732,627A  
CURRENT FILING DATE: 2000-12-08  
NUMBER OF SEQ ID NOS: 4930  
SEQ ID NO: 4287  
LENGTH: 390  
TYPE: DNA  
ORGANISM: Gossypium hirsutum  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3493-028-P1-M1-F9  
US-09-732-627A-4287

Query Match 2.1%; Score 23; DB 11; Length 390;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 ACTAAGACCGTCACGAGAGT 245  
DB 43 ACTAAGACCGTCACGAGAGT 65

RESULT 9  
US-10-021-323-15482  
Sequence 15482, Application US/100212323  
Publication No. US20040123340A1  
GENERAL INFORMATION:  
APPLICANT: Deikman, J111  
APPLICANT: Feng, Paul C.C.  
APPLICANT: Fincher, Karen L.

APPLICANT: Ziegler, Todd E.  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(52274)B  
CURRENT APPLICATION NUMBER: US/10/021,323  
CURRENT FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: US 60/255, 619  
PRIOR FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 17880  
SEQ ID NO: 15482  
LENGTH: 587  
TYPE: DNA  
ORGANISM: Gossypium hirsutum  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3829-026-Q6-K6-G6  
US-10-021-323-15482

Query Match 2.1%; Score 23; DB 18; Length 587;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 ACTAAGACCGTCACGAGAGT 245  
DB 257 ACTAAGACCGTCACGAGAGT 279

RESULT 10  
US-10-767-795-3984  
Sequence 3984, Application US/10767795  
Publication No. US20040181830A1  
GENERAL INFORMATION:  
APPLICANT: Kovalic, David K.  
APPLICANT: Cao, Yongwei  
APPLICANT: Zhou, Yihua  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(53534)B  
CURRENT APPLICATION NUMBER: US/10/767,795  
CURRENT FILING DATE: 2004-01-30  
NUMBER OF SEQ ID NOS: 117596  
SEQ ID NO: 3984  
LENGTH: 938  
TYPE: DNA  
ORGANISM: Gossypium hirsutum  
FEATURE:  
OTHER INFORMATION: Clone ID: GOSH-09MAY01-C3741\_1  
US-10-767-795-3984

Query Match 2.1%; Score 23; DB 18; Length 938;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 ACTAAGACCGTCACGAGAGT 245  
DB 258 ACTAAGACCGTCACGAGAGT 280

RESULT 11  
US-10-295-403-147  
Sequence 147, Application US/10295403  
Publication No. US20030101481A1  
GENERAL INFORMATION:  
APPLICANT: Heard, Jacqueline  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Adam, Luc  
APPLICANT: Broun, Pierre  
APPLICANT: Pineda, Omalta  
APPLICANT: Reuber, Lynne  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Keddie, James  
APPLICANT: Zhang, James  
APPLICANT: Benito, Maria-Ines  
APPLICANT: Yu, Guo-Liang

APPLICANT: Fromm, Mike  
TITLE OF INVENTION: PLANT GENE SEQUENCES I  
FILE REFERENCE: MBI-0003  
CURRENT APPLICATION NUMBER: US/10/295,403  
PRIOR FILING DATE: 2002-11-15  
PRIOR APPLICATION NUMBER: US/09/394,519  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: 60/101,349  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/103,312  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/108,734  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/113,409  
PRIOR FILING DATE: 1998-12-22  
NUMBER OF SEQ ID NOS: 170  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 147  
LENGTH: 1604  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (143)..(1345)  
OTHER INFORMATION: G802  
US-10-295-403-147

Query Match 2.1% Score 23; DB 15; Length 1604;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 TCGACTTAAAGACCGTCACACGAA 242  
DB 317 TCGACTTAAAGACCGTCACACGAA 339

RESULT 12  
US-10-412-699B-551  
Sequence 551, Application US/10412699B  
Publication No. US20040045049A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Zhang, James  
APPLICANT: Fromm, Michael E.  
APPLICANT: Heard, Jacqueline E.  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Adam, Luc J.  
APPLICANT: Broun, Pierre E.  
APPLICANT: Pineda, Omatia  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddie, James S.  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Samaha, Raymond R.  
APPLICANT: Pilgrim, Marsha L.  
APPLICANT: Creelman, Robert A.  
APPLICANT: Dubell, Arnold N.  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Kumimoto, Bradley K.  
APPLICANT: Sherman, Bradley K.  
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants  
FILE REFERENCE: MBI-0048CIP  
CURRENT APPLICATION NUMBER: US/10/412,699B  
CURRENT FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: 09/394,519  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: 09/489,376  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: 09/506,720  
PRIOR FILING DATE: 2000-02-17  
PRIOR APPLICATION NUMBER: 09/533,030  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,392

PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,029  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/532,591  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,648  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/713,994  
PRIOR FILING DATE: 2000-11-16  
PRIOR APPLICATION NUMBER: 09/819,142  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2011  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 551  
LENGTH: 1604  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
OTHER INFORMATION: G802  
US-10-412-699B-551

Query Match 2.1% Score 23; DB 17; Length 1604;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 TCGACTTAAAGACCGTCACACGAA 242  
DB 317 TCGACTTAAAGACCGTCACACGAA 339

RESULT 13  
US-10-363-345A-33693/C  
Sequence 33693, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
TITLE OF INVENTION: Method for determining the degree of methylation of defined  
FILE REFERENCE: E01/1227  
CURRENT APPLICATION NUMBER: US/10/363,345A  
CURRENT FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 40712  
SEQ ID NO 33693  
LENGTH: 755  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-363-345A-33693

Query Match 2.0% Score 21; DB 18; Length 755;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 AAAAATCCCGACGACGACGAA 458  
DB 88 AAAAATCCCGACGACGACGAA 68

RESULT 14  
US-10-363-345A-33694  
Sequence 33694, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
APPLICANT: Kurt Berlin  
TITLE OF INVENTION: Method for determining the degree of methylation of defined  
FILE REFERENCE: cytosines in genomic DNA in the sequence context of 5'-CpG-3

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; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 33694
; LENGTH: 755
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-33694

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```

Query Match          2.0%; Score 21; DB 18; Length 755;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 438 AAAAATCCGACGACGACGAA 458
DB 668 AAAAATCCGACGACGACGAA 688

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RESULT 15
US-10-425-115-164143/C
; Sequence 164143, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: LA ROBA, Thomas J.
; APPLICANT: KOVALIC, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 164143
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_81277C.1
US-10-425-115-164143

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Query Match          1.9%; Score 20; DB 18; Length 432;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 767 CCGCTGCTTCGCGCTGCT 786
DB 289 CCGCTGCTTCGCGCTGCT 270

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Search completed: February 28, 2005, 12:54:07  
 Job time : 675.967 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2005, 12:00:51 ; Search time 330.152 Seconds  
(without alignments)  
8311.439 Million cell updates/sec

Title: US-09-938-842a-3729

Perfect score: 1677

Sequence: 1 ggttaagcgttactatg.....ttctctcagctatctta 1677

Scoring table: OLIGO-MUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Size: 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*

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2: /cgn2\_6/pdata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/pdata/1/ina/RA.COMB.seq:\*  
4: /cgn2\_6/pdata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/pdata/1/ina/6B.PCTUS.COMB.seq:\*  
6: /cgn2\_6/pdata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19	1.1	400	4 US-08-956-171E-3898	Sequence 3898, Ap
C 2	19	1.1	400	4 US-08-781-986A-3898	Sequence 3898, Ap
C 3	19	1.1	601	4 US-09-949-016-23701	Sequence 23701, A
C 4	19	1.1	601	4 US-09-949-016-163444	Sequence 163444, A
C 5	19	1.1	7563	4 US-08-956-171E-33	Sequence 33, Appl
C 6	19	1.1	7563	4 US-08-781-986A-33	Sequence 33, Appl
C 7	19	1.1	85869	4 US-09-949-016-12017	Sequence 12017, A
C 8	19	1.1	85878	4 US-09-949-016-16321	Sequence 16321, A
C 9	19	1.1	90724	4 US-09-949-016-16601	Sequence 16601, A
C 10	19	1.1	94095	4 US-09-949-016-14389	Sequence 14389, A
C 11	19	1.1	177293	4 US-09-949-016-16313	Sequence 16313, A
C 12	19	1.1	321022	4 US-09-949-016-11852	Sequence 11852, A
C 13	19	1.1	321022	4 US-09-949-016-14166	Sequence 14166, A
C 14	19	1.1	342	4 US-10-121-857-58	Sequence 58, Appl
C 15	18	1.1	493	4 US-09-270-767-3134	Sequence 3134, Ap
C 16	18	1.1	493	4 US-09-270-767-18416	Sequence 18416, A
C 17	18	1.1	601	4 US-09-949-016-136404	Sequence 136404, A
C 18	18	1.1	601	4 US-09-949-016-136405	Sequence 136405, A
C 19	18	1.1	601	4 US-09-949-016-205108	Sequence 205108, A
C 20	18	1.1	832	2 US-08-461-5928-6	Sequence 6, Appl
C 21	18	1.1	832	2 US-09-198-119C-48	Sequence 48, Appl
C 22	18	1.1	876	4 US-09-601-802D-48	Sequence 48, Appl
C 23	18	1.1	876	4 US-09-601-802D-48	Sequence 48, Appl
C 24	18	1.1	877	3 US-09-198-119C-72	Sequence 72, Appl
C 25	18	1.1	877	3 US-09-601-802D-72	Sequence 72, Appl
C 26	18	1.1	887	3 US-09-198-119C-68	Sequence 68, Appl
C 27	18	1.1	887	4 US-09-601-802D-68	Sequence 68, Appl

C 28	18	1.1	949	4 US-09-270-767-25118	Sequence 25118, A
C 29	18	1.1	1028	3 US-09-249-180-1	Sequence 1, Appl
C 30	18	1.1	1132	3 US-09-198-119C-56	Sequence 56, Appl
C 31	18	1.1	1132	4 US-09-601-802D-56	Sequence 56, Appl
C 32	18	1.1	1163	3 US-09-249-180-5	Sequence 5, Appl
C 33	18	1.1	1185	4 US-09-134-000C-927	Sequence 927, Appl
C 34	18	1.1	1235	4 US-09-270-767-9828	Sequence 9828, Ap
C 35	18	1.1	1380	4 US-09-543-681A-2115	Sequence 2115, Ap
C 36	18	1.1	1496	4 US-09-895-652A-2	Sequence 2, Appl
C 37	18	1.1	2148	4 US-09-328-352-2704	Sequence 2704, Ap
C 38	18	1.1	5070	4 US-09-853-450-44	Sequence 44, Appl
C 39	18	1.1	18031	4 US-09-902-540-1180	Sequence 1180, Ap
C 40	18	1.1	22914	4 US-09-949-016-12489	Sequence 12489, A
C 41	18	1.1	22914	4 US-09-949-016-15613	Sequence 15613, A
C 42	18	1.1	26711	4 US-09-949-016-14214	Sequence 14214, A
C 43	18	1.1	32104	4 US-09-949-016-14722	Sequence 14722, A
C 44	18	1.1	53789	4 US-09-949-016-12137	Sequence 12137, A
C 45	18	1.1	53789	4 US-09-949-016-13955	Sequence 13955, A

#### ALIGNMENTS

RESULT 1  
US-08-956-171E-3898/C

Sequence 3898, Application US/08956171E

Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunesh

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Farnon

TITLE OF INVENTION: *Staphylococcus aureus Polynucleotides and Sequences*

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb storage

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 3898:

SEQUENCE CHARACTERISTICS:

LENGTH: 400 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

US-08-956-171E-3898

Query Match 1.1% Score 19; DB 4; Length 400;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 TTGTTGAATGCTTTTCA 67  
Db 129 TTGTTGAATGCTTTTCA 111

## RESULT 2

US-08-781-986A-3898/c  
Sequence 3898, Application US/08781986A  
Patent No. 6737248

GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248BP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 3898:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 400 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-3898

Query Match 1.1% Score 19; DB 4; Length 400;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 TTGTTGAATGCTTTTCA 67  
Db 129 TTGTTGAATGCTTTTCA 111

## RESULT 3

US-09-949-016-23701/c  
Sequence 23701, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 23701  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-23701

Query Match 1.1% Score 19; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1317 CAATTAAGAAACATTT 1335  
Db 43 CAATTAAGAAACATTT 25

## RESULT 4

US-09-949-016-163444/c  
Sequence 163444, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 163444  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-163444

Query Match 1.1% Score 19; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1317 CAATTAAGAAACATTT 1335  
Db 43 CAATTAAGAAACATTT 25

## RESULT 5

US-08-956-171E-33/c  
Sequence 33, Application US/08956171E  
Patent No. 6593114

GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland

COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7563 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-08-956-171E-33

Query Match 1.1%; Score 19; DB 4; Length 7563;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 49 TTGTTGAATGCTTTTCA 67  
Db 2292 TTGTTGAATGCTTTTCA 2274

RESULT 6  
US-08-781-986A-33/c  
Sequence 33, Application US/08781986A  
Patent No. 6737248  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446  
REFERENCE/DOCKET NUMBER: PB248PP  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7563 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-781-986A-33

Query Match 1.1%; Score 19; DB 4; Length 7563;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 49 TTGTTGAATGCTTTTCA 67  
Db 2292 TTGTTGAATGCTTTTCA 2274

RESULT 7  
US-09-949-016-12017  
Sequence 12017, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12017  
LENGTH: 85869  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-12017

Query Match 1.1%; Score 19; DB 4; Length 85869;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1317 CATATAAGAAAACATTT 1335  
Db 65772 CATATAAGAAAACATTT 65790

RESULT 8  
US-09-949-016-16321  
Sequence 16321, Application US/09949016  
Patent No. 6812338  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16321

LENGTH: 85878  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-16321

Query Match  
Best Local Similarity 1.1%; Score 19; DB 4; Length 85878;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1317 CATATAAGAAAAACATT 1335  
DB 65772 CATATAAGAAAAACATT 65790

RESULT 9  
US-09-949-016-16601

Sequence 16601, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16601

LENGTH: 90724

TYPE: DNA

ORGANISM: Human

US-09-949-016-16601

Query Match  
Best Local Similarity 1.1%; Score 19; DB 4; Length 90724;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1259 GTTTCGATTGATTTT 1277  
DB 42588 GTTTCGATTGATTTT 42606

LT 10

US-09-949-016-14389/c

Sequence 14389, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14389

LENGTH: 94095

TYPE: DNA

ORGANISM: Human

FEATURE:  
NAME/KEY: misc\_feature

LOCATION: (1)...(94095)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14389

Query Match  
Best Local Similarity 1.1%; Score 19; DB 4; Length 94095;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AATGCTTCAGGCTTTTGT 118  
DB 68048 AATGCTTCAGGCTTTTGT 68030

RESULT 11

US-09-949-016-16513  
Sequence 16513, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16513

LENGTH: 177293

TYPE: DNA

ORGANISM: Human

US-09-949-016-16513

Query Match  
Best Local Similarity 1.1%; Score 19; DB 4; Length 177293;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 TTTTCATTAATTAAGT 1110  
DB 117431 TTTTCATTAATTAAGT 117449

RESULT 12

US-09-949-016-11852

Sequence 11852, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11852

LENGTH: 321022

TYPE: DNA

ORGANISM: Human

FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(321022)

OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-11852

Query Match 1.1%; Score 19; DB 4; Length 321022;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TGCTTTTCAGATCATCAA 76  
DB 283681 TGCTTTTCAGATCATCAA 283699

RESULT 13  
US-09-949-016-14166

; Sequence 14166, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14166  
; LENGTH: 321022  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(321022)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14166

Query Match 1.1%; Score 19; DB 4; Length 321022;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 TGCTTTTCAGATCATCAA 76  
DB 283681 TGCTTTTCAGATCATCAA 283699

RESULT 14  
US-10-121-857-58

; Sequence 58, Application US/10121857  
; Patent No. 6822141  
; GENERAL INFORMATION:  
; APPLICANT: Lardizabal, Kathryn D  
; APPLICANT: Hawkins, Deborah J  
; APPLICANT: Thompson, Gregory A  
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins  
; FILE REFERENCE: 16515.143  
; CURRENT APPLICATION NUMBER: US/10/121,857  
; CURRENT FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: US 09/345,461  
; PRIOR FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: US 60/091,631  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: US 60/130,829  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 342  
; TYPE: DNA

ORGANISM: murine  
US-10-121-857-58

Query Match 1.1%; Score 18; DB 4; Length 342;  
Best Local Similarity 100.0%; Pred. No. 81;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1186 TGAATTTTGTACCAA 1203  
DB 267 TGAATTTTGTACCAA 284

RESULT 15  
US-09-270-767-3134

; Sequence 3134, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3134  
; LENGTH: 493  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-3134

Query Match 1.1%; Score 18; DB 4; Length 493;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1104 TTAAGTAATCTTTT 1121  
DB 363 TTAAGTAATCTTTT 380

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Job time : 333.152 secs

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OM nucleic - nucleic search, using sw model

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(without alignment)

9423.127 Million cell updates/sec

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13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*  
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21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	23	1.4	174448	US-10-087-192-148	Sequence 148, Ap
4	21	1.3	330	US-09-930-213-54	Sequence 54, Appl
5	21	1.3	394	US-09-803-719-707	Sequence 707, App
6	21	1.3	406	US-10-424-599-103891	Sequence 103891, App
7	21	1.3	407	US-09-803-719-1633	Sequence 1633, Ap
8	21	1.3	2000	US-10-191-807-3	Sequence 306, Appl
9	21	1.3	108359	US-10-367-094-114	Sequence 114, App
10	21	1.3	133462	US-10-027-632-54726	Sequence 54726, A
11	20	1.2	627	US-10-027-632-54726	Sequence 54726, A

C 12	20	1.2	627	13	US-10-027-632-294129	Sequence 294129, A
C 13	20	1.2	627	17	US-10-027-632-54726	Sequence 54726, A
C 14	20	1.2	627	17	US-10-027-632-284129	Sequence 284129, A
C 15	20	1.2	628	18	US-10-437-963-9063	Sequence 9063, Ap
C 16	20	1.2	768	9	US-09-815-242-9987	Sequence 9987, Ap
C 17	20	1.2	768	17	US-10-282-122A-39631	Sequence 39631, A
C 18	20	1.2	769	17	US-10-282-122A-36869	Sequence 36869, A
C 19	20	1.2	1793	17	US-10-424-599-63060	Sequence 63060, A
C 20	20	1.2	6059	18	US-10-437-963-70677	Sequence 70677, A
C 21	20	1.2	6449	18	US-10-437-963-101721	Sequence 101721, A
C 22	20	1.1	199	16	US-10-029-386-14103	Sequence 14103, A
C 23	19	1.1	281	17	US-10-242-5352A-18166	Sequence 18166, A
C 24	19	1.1	281	17	US-10-085-783A-18166	Sequence 18166, A
C 25	19	1.1	307	18	US-10-437-963-26666	Sequence 26666, A
C 26	19	1.1	377	9	US-09-983-965-5678	Sequence 5678, Ap
C 27	19	1.1	400	8	US-08-781-986A-3898	Sequence 3898, Ap
C 28	19	1.1	400	17	US-10-329-624-3898	Sequence 3898, Ap
C 29	19	1.1	502	18	US-10-437-963-55251	Sequence 55251, A
C 30	19	1.1	547	16	US-10-029-386-398	Sequence 398, App
C 31	19	1.1	588	13	US-10-027-632-88862	Sequence 88862, A
C 32	19	1.1	588	13	US-10-027-632-88863	Sequence 88863, A
C 33	19	1.1	588	17	US-10-027-632-88862	Sequence 88862, A
C 34	19	1.1	588	17	US-10-027-632-88863	Sequence 88863, A
C 35	19	1.1	598	13	US-10-027-632-230239	Sequence 230239, A
C 36	19	1.1	598	13	US-10-027-632-230240	Sequence 230240, A
C 37	19	1.1	598	17	US-10-027-632-230239	Sequence 230239, A
C 38	19	1.1	598	17	US-10-027-632-230240	Sequence 230240, A
C 39	19	1.1	652	13	US-10-027-632-133067	Sequence 133067, A
C 40	19	1.1	652	17	US-10-027-632-133067	Sequence 133067, A
C 41	19	1.1	672	13	US-10-027-632-34038	Sequence 34038, A
C 42	19	1.1	753	18	US-10-027-632-34038	Sequence 34038, A
C 43	19	1.1	903	9	US-09-815-242-2975	Sequence 2975, Ap
C 44	19	1.1	903	17	US-10-282-122A-5549	Sequence 5549, Ap
C 45	19	1.1	903	17	US-10-282-122A-5549	Sequence 5549, Ap

#### ALIGNMENTS

RESULT 1  
US-09-938-842a-3729  
; Sequence 3729, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Krepes, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPT1300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 3729  
; LENGTH: 1677  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; US-09-938-842a-3729

Query Match 100.0% Score 1677; DB 9; Length 1677;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ggttaagcgtttactatggtttatgcaacgaagatattgcatgttggaatcc 60  
Db 1 ggttaagcgtttactatggtttatgcaacgaagatattgcatgttggaatcc 60

QY 61 TTTTCAGATCATCAAGGCTCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTGTTA 120  
DB 61 TTTTCAGATCATCAAGGCTCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTGTTA 120  
QY 121 GAAATGTGTTTATTCGAAACAGGTAGAGAACATTAACCATAGACAGATGTATCTGAAGAGA 180  
DB 121 GAAATGTGTTTATTCGAAACAGGTAGAGAACATTAACCATAGACAGATGTATCTGAAGAGA 180  
QY 181 TAACTTCTATGTCTTAAAGAAATGAGACGATACGAAATTAACAAGCATCTTAAGAT 240  
DB 181 TAACTTCTATGTCTTAAAGAAATGAGACGATACGAAATTAACAAGCATCTTAAGAT 240  
QY 241 TAAATGTTTGTAAAGAAATACTACATTAATTAATGAAATGTGTAGTGAAGAGT 300  
DB 241 TAAATGTTTGTAAAGAAATACTACATTAATTAATGAAATGTGTAGTGAAGAGT 300  
QY 301 AAAAATCATGGGAATCCAAAACCTCAATTTACCAATCAAGCCCAATTAATGATGCTGCG 360  
DB 301 AAAAATCATGGGAATCCAAAACCTCAATTTACCAATCAAGCCCAATTAATGATGCTGCG 360  
QY 361 TAAATGATGTATGTCTGATGTAGGCAAAAAGTTGGTGGTGGCAAAATTAACAACATATC 420  
DB 361 TAAATGATGTATGTCTGATGTAGGCAAAAAGTTGGTGGTGGCAAAATTAACAACATATC 420  
QY 421 CCTGTGTGTGACCCGGAATCTGTAATCGAAAAGGTGAAACCACTTGTTTAACTTTT 480  
DB 421 CCTGTGTGTGACCCGGAATCTGTAATCGAAAAGGTGAAACCACTTGTTTAACTTTT 480  
QY 481 AAGCTTAAAGGTACTACCGGTTGACCGGTTTAAATTTGGTGTAAATCTTAATCCC 540  
DB 481 AAGCTTAAAGGTACTACCGGTTGACCGGTTTAAATTTGGTGTAAATCTTAATCCC 540  
QY 541 GGATCCGTTTGTGTTTAACTCAAGGCGCATTAATGCAATTTTGAATTTTGAATG 600  
DB 541 GGATCCGTTTGTGTTTAACTCAAGGCGCATTAATGCAATTTTGAATTTTGAATG 600  
QY 601 GGTAGGGAATGGTGGGTGCAATAGTTGGGCTTACCCCTCAACAATGTGGAACGAG 660  
DB 601 GGTAGGGAATGGTGGGTGCAATAGTTGGGCTTACCCCTCAACAATGTGGAACGAG 660  
QY 661 AGAGTAGGGTCCAGTCAAGGCCCAATTCATCAATTTGTTTGAAGCTTTTCTG 720  
DB 661 AGAGTAGGGTCCAGTCAAGGCCCAATTCATCAATTTGTTTGAAGCTTTTCTG 720  
QY 721 TGCTTACGCTCCCTCTTCTGCTGCTGATGTACAGATGACATAGTGTGTTCAAA 780  
DB 721 TGCTTACGCTCCCTCTTCTGCTGCTGATGTACAGATGACATAGTGTGTTCAAA 780  
QY 781 CCCGAAACAAATGATCAAGAAATGAATGGTTGAATCGTTTACATCTAGTACGCTG 840  
DB 781 CCCGAAACAAATGATCAAGAAATGAATGGTTGAATCGTTTACATCTAGTACGCTG 840  
QY 841 AACTTCAATCATTTGATTAATCTTGAATCTGATTTCTAGTTCGTTTGAATGTTAAT 900  
DB 841 AACTTCAATCATTTGATTAATCTTGAATCTGATTTCTAGTTCGTTTGAATGTTAAT 900  
QY 901 CCGGATTTGTCAGATGACAAAGTACATTAATGTCGTAATGTATGTGACCGGTTTAAATC 960  
DB 901 CCGGATTTGTCAGATGACAAAGTACATTAATGTCGTAATGTATGTGACCGGTTTAAATC 960  
QY 961 AAAGGACGAGATGAGATTTTGAATCTGGAAGAGATTAATTCATAGACATTA 1020  
DB 961 AAAGGACGAGATGAGATTTTGAATCTGGAAGAGATTAATTCATAGACATTA 1020  
QY 1021 ATTAGCTTTTGTGGGCGACGCTTGTGACATTAATGAGGATCCAAACCCCAAGTATG 1080  
DB 1021 ATTAGCTTTTGTGGGCGACGCTTGTGACATTAATGAGGATCCAAACCCCAAGTATG 1080  
QY 1081 GGCTTACAGCTTTTTCATTAATAATTAAGTAATCTTTTTCCTTAACCAATTAAT 1140  
DB 1081 GGCTTACAGCTTTTTCATTAATAATTAAGTAATCTTTTTCCTTAACCAATTAAT 1140

QY 1141 ATTGAATATCTTTCACCAACATAGAAAAGTTAAATTTGATCAGCGATGAAAATTTTGTAC 1200  
DB 1141 ATTGAATATCTTTCACCAACATAGAAAAGTTAAATTTGATCAGCGATGAAAATTTTGTAC 1200  
QY 1201 AAAGCTAGGATTTTCAATTTGGGAGTGTACTAGTAACATAGTAATTAACCAAGATGACT 1260  
DB 1201 AAAGCTAGGATTTTCAATTTGGGAGTGTACTAGTAACATAGTAATTAACCAAGATGACT 1260  
QY 1261 TTCTGATTTTGAATTTTGAAGCTTTTCTAGTTTAAAAAACAAGTATTAATTAACAAT 1320  
DB 1261 TTCTGATTTTGAATTTTGAAGCTTTTCTAGTTTAAAAAACAAGTATTAATTAACAAT 1320  
QY 1321 AAAAAGAAAACATTTTGTGAAAAGAGAAATTAAGTTTACGTGACCCCATTTGACAGATG 1380  
DB 1321 AAAAAGAAAACATTTTGTGAAAAGAGAAATTAAGTTTACGTGACCCCATTTGACAGATG 1380  
QY 1381 TCCCATTAATATCTGATAGAAATGATAGCAATGAAAGTAAATTTGTACCGGTGACAA 1440  
DB 1381 TCCCATTAATATCTGATAGAAATGATAGCAATGAAAGTAAATTTGTACCGGTGACAA 1440  
QY 1441 TCGGAATGTTCTTTTAAAGCTCATCGAACACATCAGAACCGTTGATTTTCCCGCATCAA 1500  
DB 1441 TCGGAATGTTCTTTTAAAGCTCATCGAACACATCAGAACCGTTGATTTTCCCGCATCAA 1500  
QY 1501 AAAGCTGAAATCTATTCATCTGCTTTCCTGCTCCATTAATTAATCTGACGAGATC 1560  
DB 1501 AAAGCTGAAATCTATTCATCTGCTTTCCTGCTCCATTAATTAATCTGACGAGATC 1560  
QY 1561 ACATTTAGTAATCTCCTTGAAGCGTGTACGCGGTTAAACGATCTTCCATTTGATCC 1620  
DB 1561 ACATTTAGTAATCTCCTTGAAGCGTGTACGCGGTTAAACGATCTTCCATTTGATCC 1620  
QY 1621 GCTTTTAAACATCTCGTGTGATCTCCACCGCTCCGTTTCTCTCACTAATTTTGA 1677  
DB 1621 GCTTTTAAACATCTCGTGTGATCTCCACCGCTCCGTTTCTCTCACTAATTTTGA 1677

RESULT 2  
US-09-938-842A-3729  
; Publication 3729, Application US/09938842A  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SAME, AND METHODS OF USE  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 3729  
; LENGTH: 1677  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-3729

Query Match 100.0%; Score 1677; DB 11; Length 1677;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAAAGCGTTTATCTTATGTTATGCAACGGAAGATTAATGCAATGTTGGAATGC 60  
DB 1 GGTAAAGCGTTTATCTTATGTTATGCAACGGAAGATTAATGCAATGTTGGAATGC 60  
QY 61 TTTTCAGATCATCAAGGCTCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTGTTA 120

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Db      61 TTTTCAGATCATCAAGGCTCCTACAGTTTCTTAGGAAATGTTTTCAGGCTTTTGTA 120
Qy      121 GAAATTTGTTTATTTGCAACAGGTAGAGAAATTAACCATAGACAGATGTAATCGAAGAGA 180
Db      121 GAAATTTGTTTATTTGCAACAGGTAGAGAAATTAACCATAGACAGATGTAATCGAAGAGA 180
Qy      181 TAGGCTTCTATGCTAATAGAAATGAGACCGAATGCAATTAACCAAGCATCTTAAGAT 240
Db      181 TAGGCTTCTATGCTAATAGAAATGAGACCGAATGCAATTAACCAAGCATCTTAAGAT 240
Qy      241 TAAATGTTTGTAAAGAAATACACTTATTAATGAAATGTTGTTAGTGAAGAT 300
Db      241 TAAATGTTTGTAAAGAAATACACTTATTAATGAAATGTTGTTAGTGAAGAT 300
Qy      301 AAAAATCATCGAATCCAAACCTCAAAATTTACCAATGAGCCCAATTTATGATGCTGGC 360
Db      301 AAAAATCATCGAATCCAAACCTCAAAATTTACCAATGAGCCCAATTTATGATGCTGGC 360
Qy      361 TAAATGATGTTATGCTGATAGTAAAGGAAATGTTGCTGCGAAATTAACCAATATC 420
Db      361 TAAATGATGTTATGCTGATAGTAAAGGAAATGTTGCTGCGAAATTAACCAATATC 420
Qy      421 CCTCTGTGTGACCCGGAATCTGTATCGGAAAGGTTGAAACCCACTTGTGTTAACTTT 480
Db      421 CCTCTGTGTGACCCGGAATCTGTATCGGAAAGGTTGAAACCCACTTGTGTTAACTTT 480
Qy      481 AAGCTTAAAGGTTTACTACCGGTTTGAACGGTTTAAATTTGTTAAATCTTAATCCC 540
Db      481 AAGCTTAAAGGTTTACTACCGGTTTGAACGGTTTAAATTTGTTAAATCTTAATCCC 540
Qy      541 GGATCCGTTTGTGTTTAAATCTCAAGGCAACGTTATCGCAATTTTAAATTTTAAAGG 600
Db      541 GGATCCGTTTGTGTTTAAATCTCAAGGCAACGTTATCGCAATTTTAAATTTTAAAGG 600
Qy      601 GGTAGGGAATGTTGGGGTGGAAATAGTTGGGCTAGCCCTCAACAATGTGTGAACGTAAG 660
Db      601 GGTAGGGAATGTTGGGGTGGAAATAGTTGGGCTAGCCCTCAACAATGTGTGAACGTAAG 660
Qy      661 AAGATGAGGTTCCAGCTCAGAGCCCAATTCATATTTGTTTGTAGCCCTTTCTTTCTG 720
Db      661 AAGATGAGGTTCCAGCTCAGAGCCCAATTCATATTTGTTTGTAGCCCTTTCTTTCTG 720
Qy      721 TGTCTTACGGTCCCTCTTTCTGTGCGGTGCTATGTACAAAGTAAAGTAAAGTAAAGT 780
Db      721 TGTCTTACGGTCCCTCTTTCTGTGCGGTGCTATGTACAAAGTAAAGTAAAGTAAAGT 780
Qy      781 CCCGAAACAAGTACCAACGATCAAAATAGTTGAATCGGTTACATCTAGTTACCGTGC 840
Db      781 CCCGAAACAAGTACCAACGATCAAAATAGTTGAATCGGTTACATCTAGTTACCGTGC 840
Qy      841 AACTTACATCAATTTGATTAATCTTATGATCTGATTTCTAGTTGCGTTTGTATGTTAAT 900
Db      841 AACTTACATCAATTTGATTAATCTTATGATCTGATTTCTAGTTGCGTTTGTATGTTAAT 900
Qy      901 CCGGATTTGTAAGTACCAAGTAAATGATGATGATGATGATGATGATGATGATGATGAT 960
Db      901 CCGGATTTGTAAGTACCAAGTAAATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy      961 AAAGGACGAGTAAAGGATTTTGAATCTCGAAAGAGATTTTTCATAGACACTA 1020
Db      961 AAAGGACGAGTAAAGGATTTTGAATCTCGAAAGAGATTTTTCATAGACACTA 1020
Qy      1021 ATTAGCTTTTGTGTGCGAGCTTGTGACTTATGATTAATGAGGCTCAACCCCAATGATG 1080
Db      1021 ATTAGCTTTTGTGTGCGAGCTTGTGACTTATGATTAATGAGGCTCAACCCCAATGATG 1080
Qy      1081 GGCTTACAGCTTTTTCATTAATTAAGTAAATCTTTTTCCTTAAACCAATTAATTAAT 1140
Db      1081 GGCTTACAGCTTTTTCATTAATTAAGTAAATCTTTTTCCTTAAACCAATTAATTAAT 1140
Qy      1141 ATTGAATCTTTCCACCATAGAAAAGTAAATTTGATCAGCATGAGAAATTTTGTAC 1200

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Db      1141 ATTGAATCTTTCCACCATAGAAAAGTAAATTTGATCAGCATGAGAAATTTTGTAC 1200
Qy      1201 AAAGCTAGGATTTTCAATTTGGAGTGTACTAATTAAGTCTAACCAGAAATGAT 1260
Db      1201 AAAGCTAGGATTTTCAATTTGGAGTGTACTAATTAAGTCTAACCAGAAATGAT 1260
Qy      1261 TTCTGATTTTGGATTTTGAAGCTTTTCTAGGTTTAAAAAACAAGTATTTACTTAAACAT 1320
Db      1261 TTCTGATTTTGGATTTTGAAGCTTTTCTAGGTTTAAAAAACAAGTATTTACTTAAACAT 1320
Qy      1321 AAAAGAAAAATTTTGTGAAAGAAATAAAGTTTACTGAGACCCCATTTGTAACATG 1380
Db      1321 AAAAGAAAAATTTTGTGAAAGAAATAAAGTTTACTGAGACCCCATTTGTAACATG 1380
Qy      1381 TCCCATTAATTAATCTGATGAGATGAGCAATGGAATGATTTGTTTCAAGGTGACAA 1440
Db      1381 TCCCATTAATTAATCTGATGAGATGAGCAATGGAATGATTTGTTTCAAGGTGACAA 1440
Qy      1441 TCGGAATGTTCTTTTAAAGCTCATCGAACACATCAGAACCGTTGATTTTCCCGCATCA 1500
Db      1441 TCGGAATGTTCTTTTAAAGCTCATCGAACACATCAGAACCGTTGATTTTCCCGCATCA 1500
Qy      1501 AAAGGTTGAATATCTATTTCTCACTTGTCTTCTGCTCTATATATATATCTGACAGATC 1560
Db      1501 AAAGGTTGAATATCTATTTCTCACTTGTCTTCTGCTCTATATATATATCTGACAGATC 1560
Qy      1561 ACATTTAGTAAATCTCTTGGAGATGTAAGCGGTTTAAACGATTTCTTCCATTTGATCC 1620
Db      1561 ACATTTAGTAAATCTCTTGGAGATGTAAGCGGTTTAAACGATTTCTTCCATTTGATCC 1620
Qy      1621 GCTTTTAAACAATCTGCTGCTCATCTCCACCGTTCCTCTCACTATATTTTA 1677
Db      1621 GCTTTTAAACAATCTGCTGCTCATCTCCACCGTTCCTCTCACTATATTTTA 1677

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RESULT 3
US-10-087-192-148/c
; Sequence 148, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 174448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (174448)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-148

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Query Match 1.4%; Score 23; DB 13; Length 174448;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      223 ACAAGCATCATTAAGATTAAT 245
Db      149367 ACAAGCATCATTAAGATTAAT 149345

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RESULT 4

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US-09-930-213-54
; Sequence 54, Application US/09930213
; Publication No. US20030170625A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAEFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHER-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELLMINGEL, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTEL
; APPLICANT: SEBS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (4)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (9)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-09-930-213-54

Query Match
Best Local Similarity 1.3%; Score 21; DB 10; Length 330;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 TTATCCCTCTGTGTGAGACC 436
DB 148 TTATCCCTCTGTGTGAGACC 168

RESULT 5
US-09-803-719-707
; Sequence 707, Application US/09803719
; Publication No. US20030044783A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Dimaac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Human Genes and Gene Products
; FILE REFERENCE: 1624.002
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US-09-938-842a-3729.olg.rnpb

; CURRENT APPLICATION NUMBER: US/09/803,719
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,609
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 2396
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 707
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-803-719-707

Query Match
Best Local Similarity 1.3%; Score 21; DB 10; Length 394;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 TTATCCCTCTGTGTGAGACC 436
DB 49 TTATCCCTCTGTGTGAGACC 69

RESULT 6
US-10-424-599-103891
; Sequence 103891, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 103891
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64830C.1
US-10-424-599-103891

Query Match
Best Local Similarity 1.3%; Score 21; DB 17; Length 406;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1139 TTATTGAAATCTTCCAAACC 1159
DB 254 TTATTGAAATCTTCCAAACC 274

RESULT 7
US-09-803-719-1633
; Sequence 1633, Application US/09803719
; Publication No. US20030044783A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassam, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
```

```

; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, Lee William
; APPLICANT: Stache-Crain, Birgit
; TITLE OF INVENTION: Human Genes and Gene Products
; FILE REFERENCE: 1624.002
; CURRENT APPLICATION NUMBER: US/09/803,719
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,609
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 2396
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1633
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-938-719-1633

Query Match
Best Local Similarity 1.3%; Score 21; DB 10; Length 407;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 TTATCCCTCTGTGTGAGACC 436
DB 195 TTATCCCTCTGTGTGAGACC 215

RESULT 8
US-09-930-213-306
; Sequence 306, Application US/09930213
; Publication No. US20030170625A1
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, ANDRE
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHAFER, REINHARD
; APPLICANT: ZUBER, JOHANNES
; APPLICANT: TCHÉ-NITSE, OLEG
; APPLICANT: GRIPS, MARTIN
; APPLICANT: HELLMER, MARTIN
; APPLICANT: SCHMITZ, ANNE-CHANTAL
; APPLICANT: SERS, CHRISTINE
; TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
; FILE REFERENCE: ALBRE-14
; CURRENT APPLICATION NUMBER: US/09/930,213
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: DE 10004102.7
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 885
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 306
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-930-213-306

Query Match
Best Local Similarity 1.3%; Score 21; DB 10; Length 2000;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 416 TTATCCCTCTGTGTGAGACC 436
DB 885 TTATCCCTCTGTGTGAGACC 905

RESULT 9
US-10-191-807-3/C
; Sequence 3, Application US/10191807
; Publication No. US20030068691A1
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al.
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; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL001275-PROV
; CURRENT APPLICATION NUMBER: US/10/191,807
; CURRENT FILING DATE: 2002-07-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 108359
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(108359)
; OTHER INFORMATION: n = A,T,C or G
; US-10-191-807-3

Query Match
Best Local Similarity 1.3%; Score 21; DB 14; Length 108359;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 TTAATGTTGTGAAGAAATA 260
DB 75869 TTAATGTTGTGAAGAAATA 75849

RESULT 10
US-10-367-094-114/C
; Sequence 114, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 133462
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(133462)
; OTHER INFORMATION: n = A,T,C or G
; US-10-367-094-114

Query Match
Best Local Similarity 1.3%; Score 21; DB 18; Length 133462;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1333 TTTTGAAAGAGAAATATA 1353
DB 62921 TTTTGAAAGAGAAATATA 62901

RESULT 11
US-10-027-632-54726/C
; Sequence 54726, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
```

```

; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54726
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(627)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-54726
```

```
Query Match          1.2%; Score 20; DB 13; Length 627;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1134 AAAAATTATTGAAATCTTT 1153
Db      508 AAAAATTATTGAAATCTTT 489
```

```

RESULT 12
US-10-027-632-294129/c
; Sequence 294129, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294129
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(627)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-294129
```

```
Query Match          1.2%; Score 20; DB 13; Length 627;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1134 AAAAATTATTGAAATCTTT 1153
Db      508 AAAAATTATTGAAATCTTT 489
```

```

RESULT 13
US-10-027-632-54726/c
; Sequence 54726, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54726
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(627)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-54726
```

```
Query Match          1.2%; Score 20; DB 17; Length 627;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1134 AAAAATTATTGAAATCTTT 1153
Db      508 AAAAATTATTGAAATCTTT 489
```

```

RESULT 14
US-10-027-632-294129/c
; Sequence 294129, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
```

PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 294129  
LENGTH: 627  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(627)  
OTHER INFORMATION: n = A,T,C or G  
US-10-027-632-294129

Query Match 1.2%; Score 20; DB 17; Length 627;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C 1134 AAAAATTATGAAATCTTT 1153  
DB 508 AAAAATTATGAAATCTTT 489

RESULT 15  
US-10-437-963-9063  
Sequence 9063, Application US/10437963  
Publication No. US2004012343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 9063  
LENGTH: 628  
TYPE: DNA  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_15514C.1  
US-10-437-963-9063

Query Match 1.2%; Score 20; DB 18; Length 628;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1154 CCACCATAGAAAAGTTAAA 1173  
DB 297 CCACCATAGAAAAGTTAAA 316

Search completed: February 28, 2005, 12:54:09  
Job time : 1057.03 secs

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